FIG. 1a

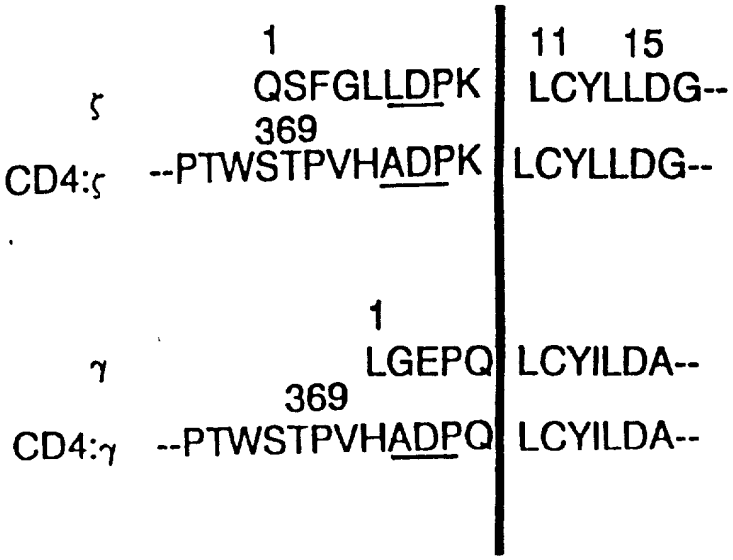


FIG. 1b

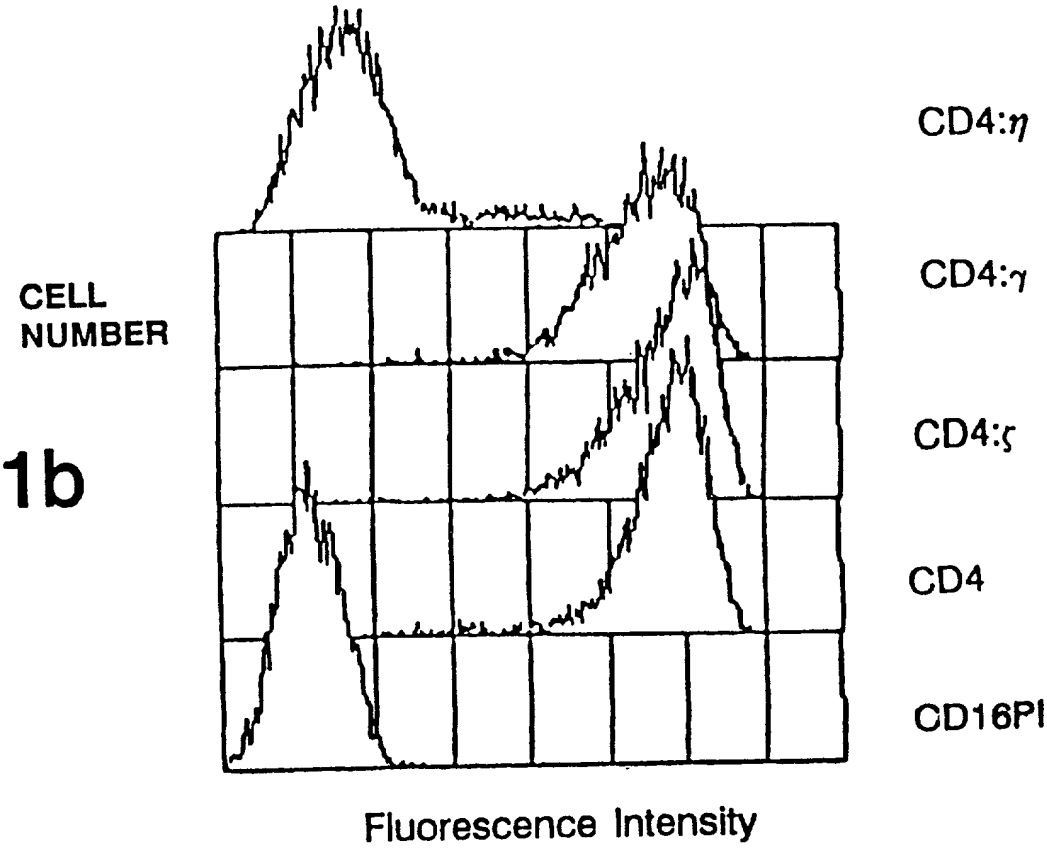


FIG. 2

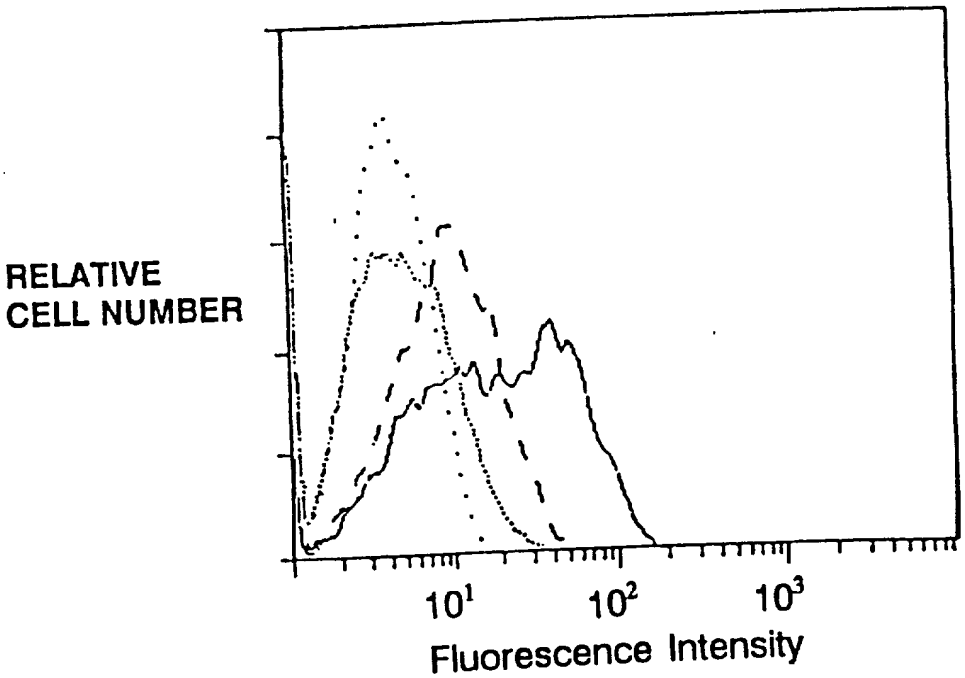

RELATIVE CELL NUMBER
10^1
10^2
10^3
Fluorescence Intensity

FIG. 3

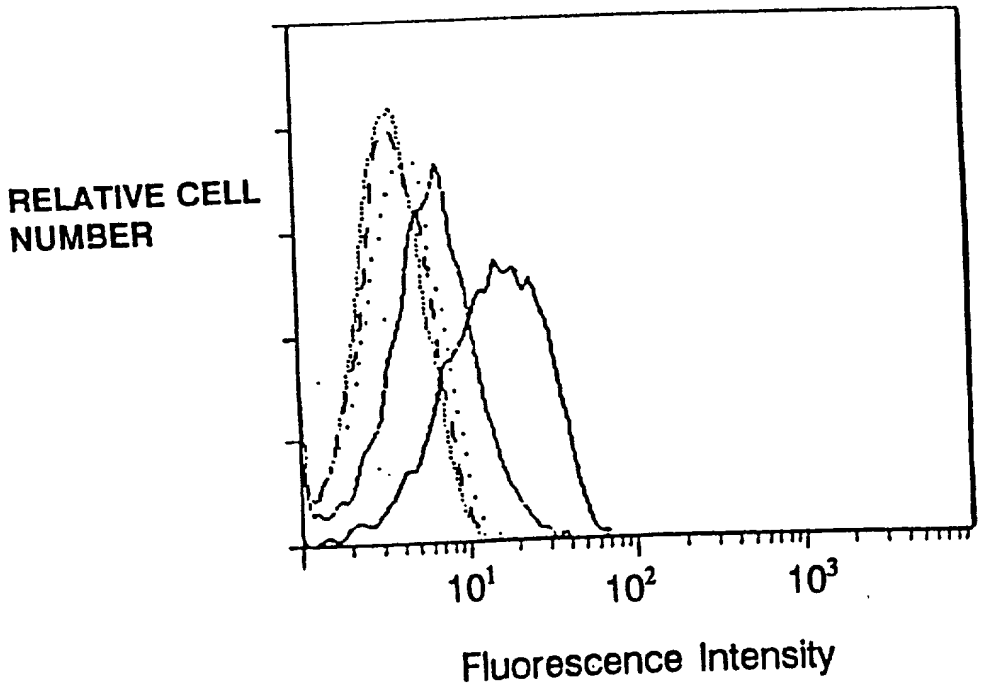

RELATIVE CELL NUMBER
10^1
10^2
10^3
Fluorescence Intensity

FIG. 4a

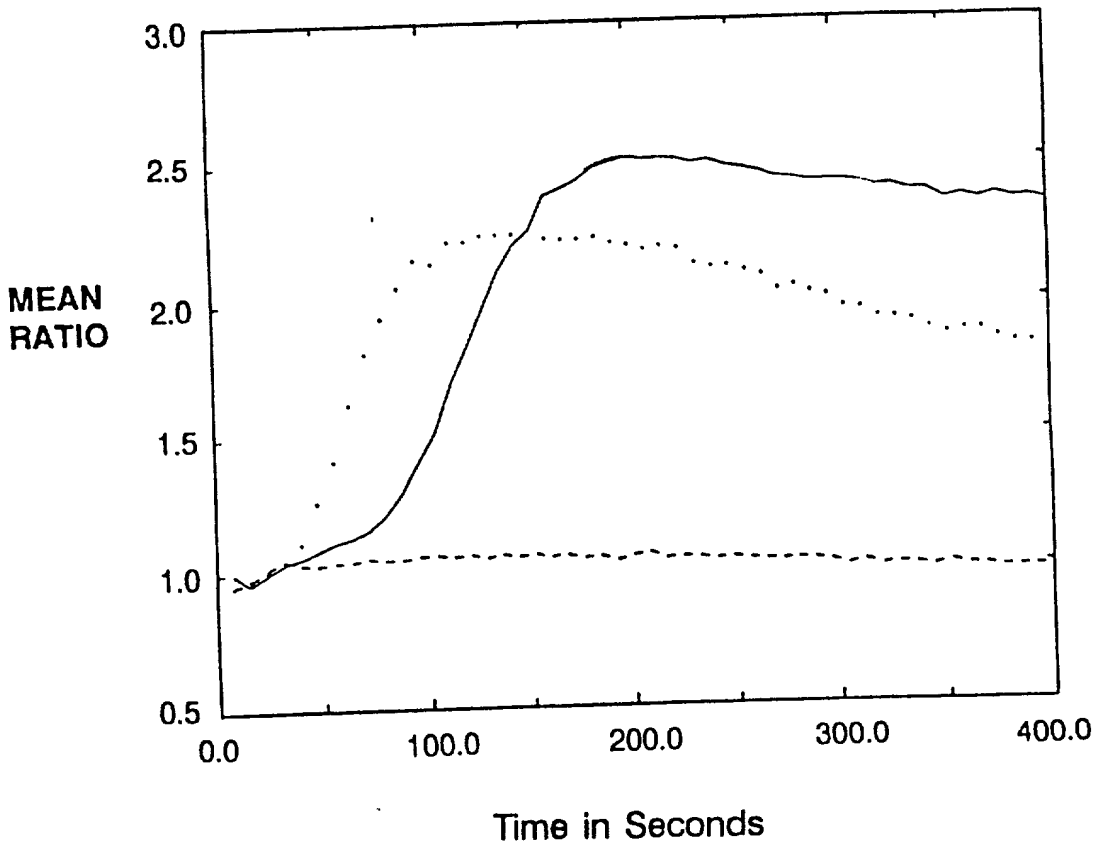

3.0
2.5
2.0
1.5
1.0
0.5
MEAN RATIO
0.0
100.0
200.0
300.0
400.0
Time in Seconds

FIG. 4b

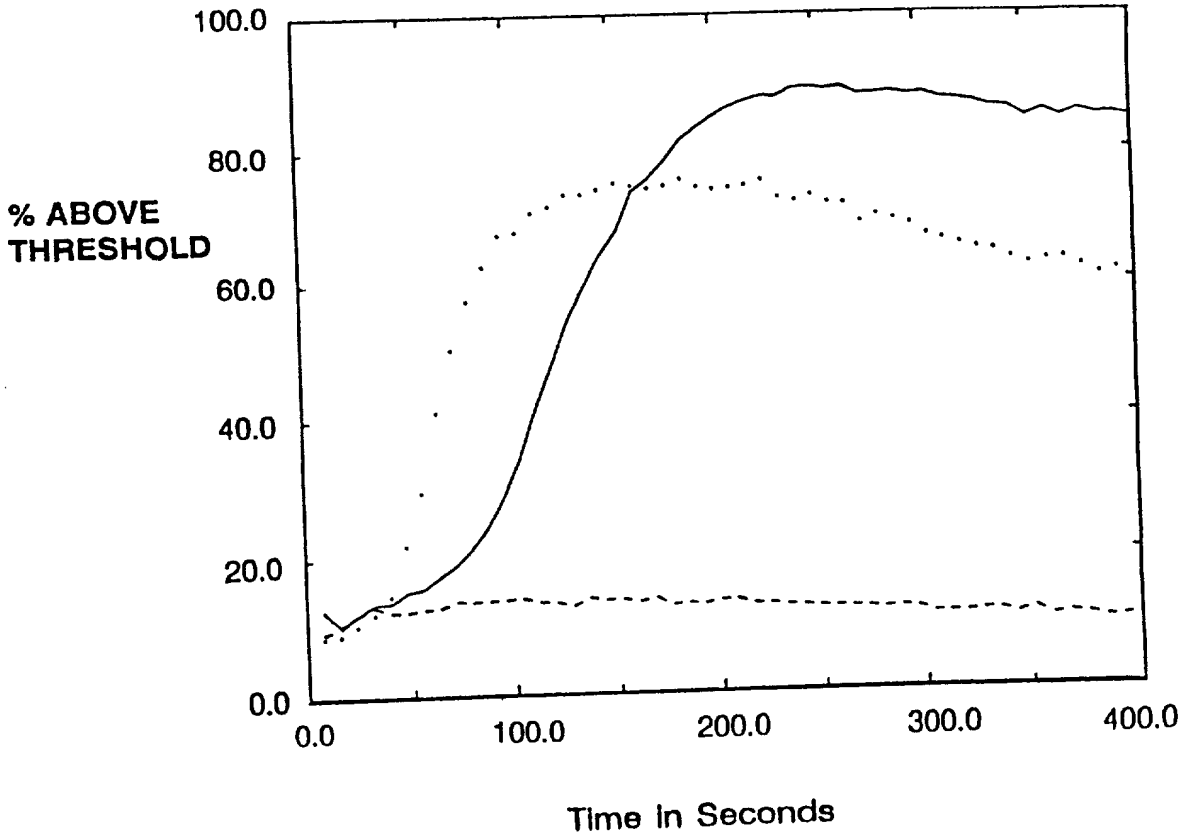

100.0
80.0
60.0
40.0
20.0
0.0
% ABOVE THRESHOLD
0.0
100.0
200.0
300.0
400.0
Time in Seconds

FIG. 4c

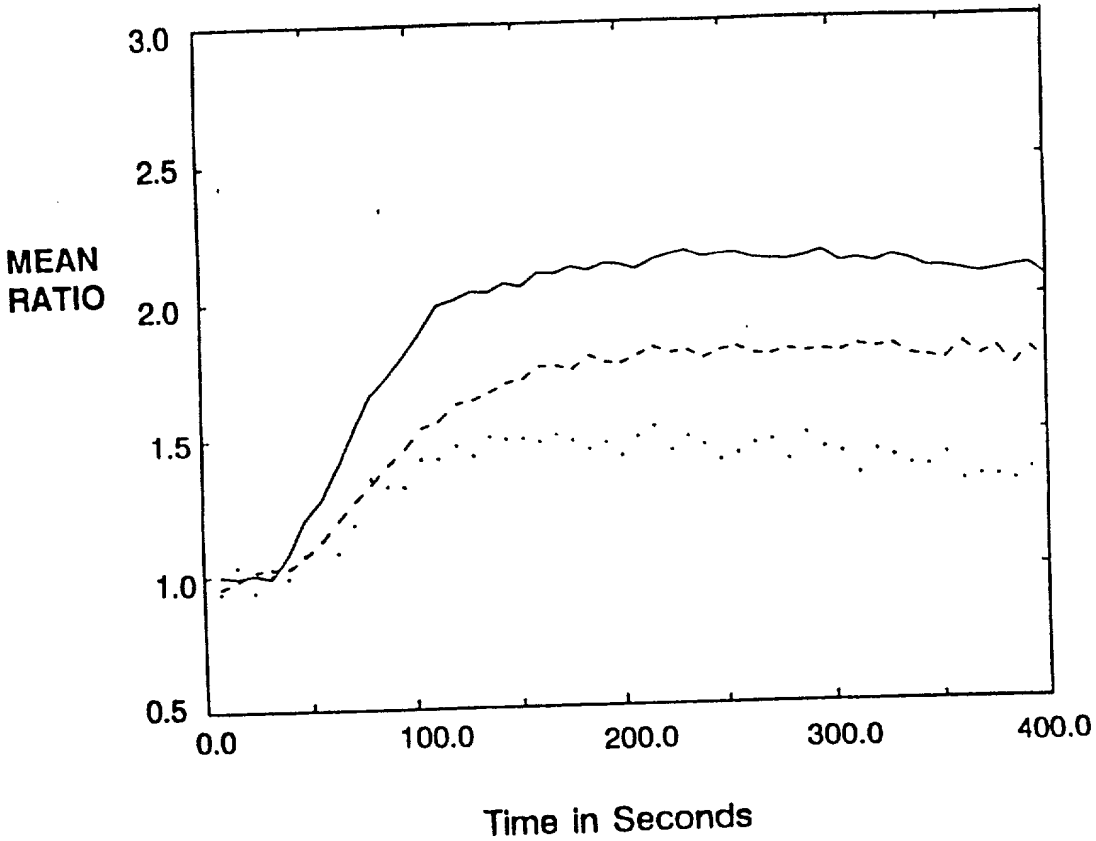

3.0
2.5
2.0
1.5
1.0
0.5
MEAN RATIO
0.0
100.0
200.0
300.0
400.0
Time in Seconds

FIG. 4d

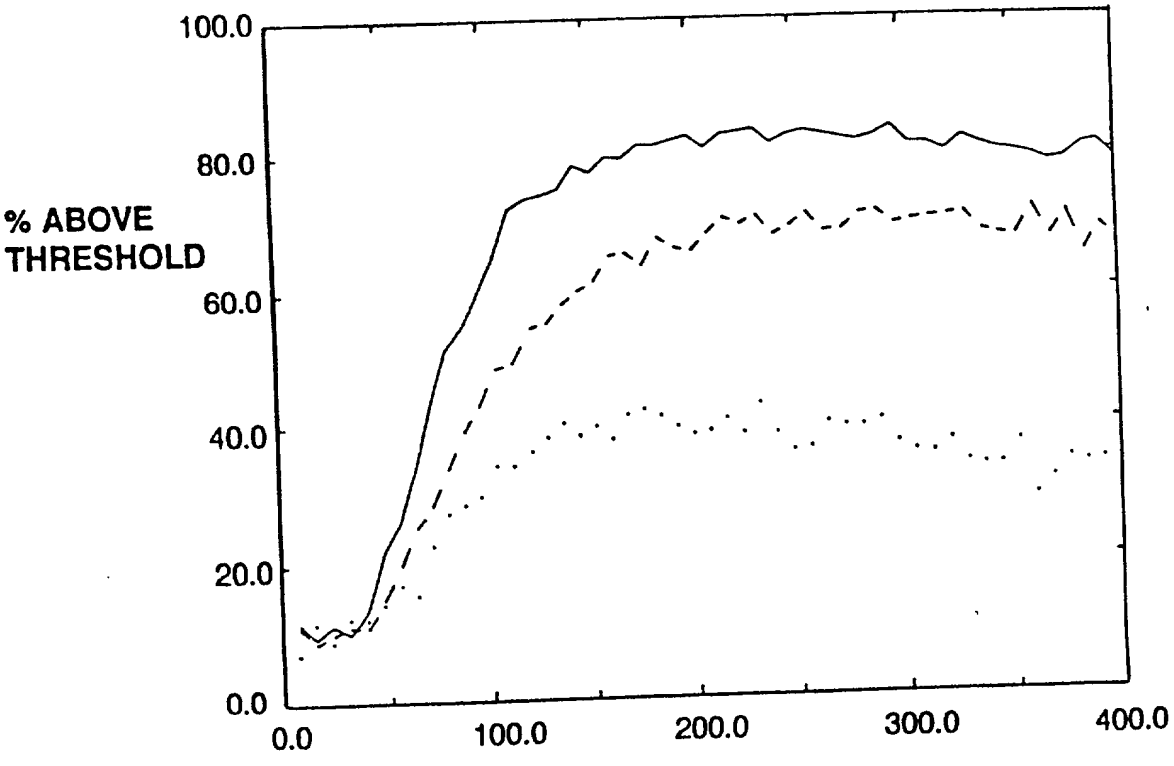

100.0
80.0
60.0
40.0
20.0
0.0
% ABOVE THRESHOLD
0.0
100.0
200.0
300.0
400.0
Time in Seconds

FIG. 5a

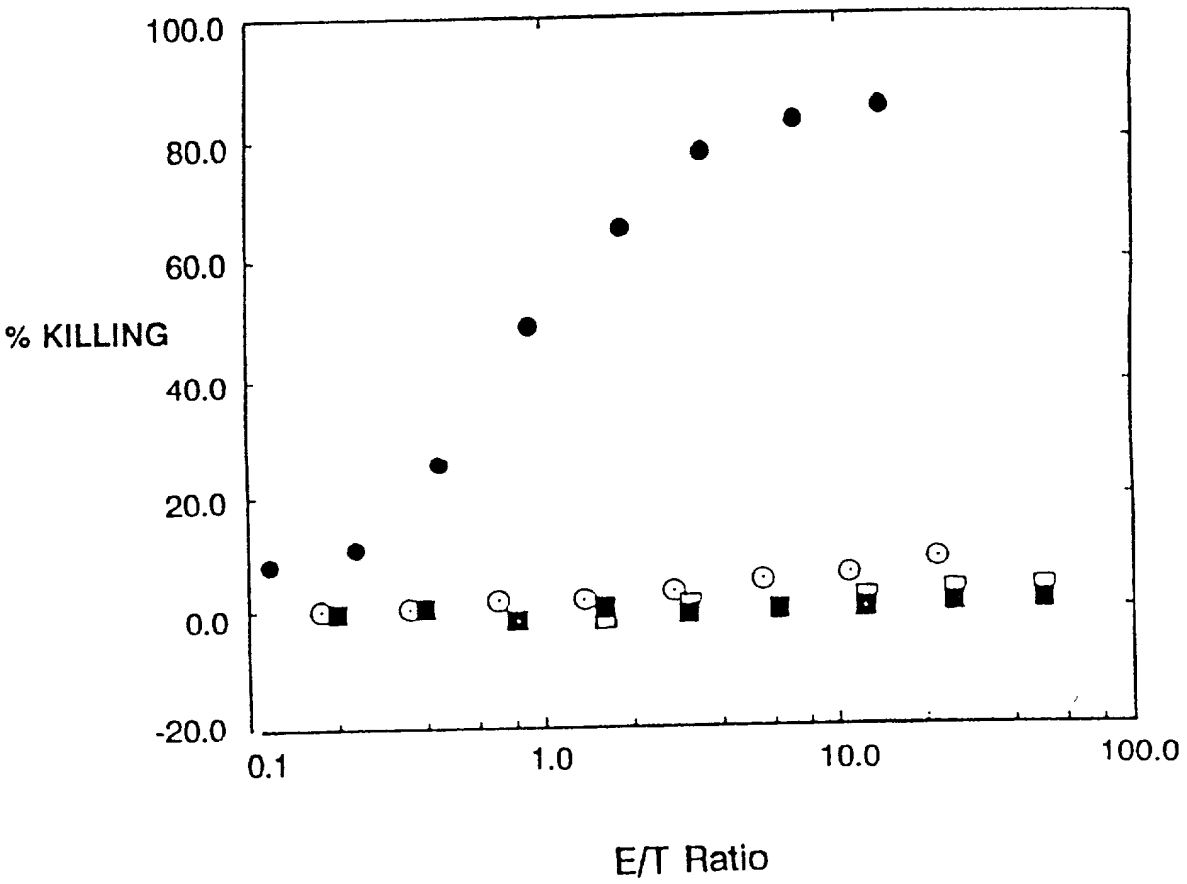

100.0
80.0
60.0
% KILLING
40.0
20.0
0.0
-20.0
0.1
1.0
10.0
100.0
E/T Ratio

FIG. 5b

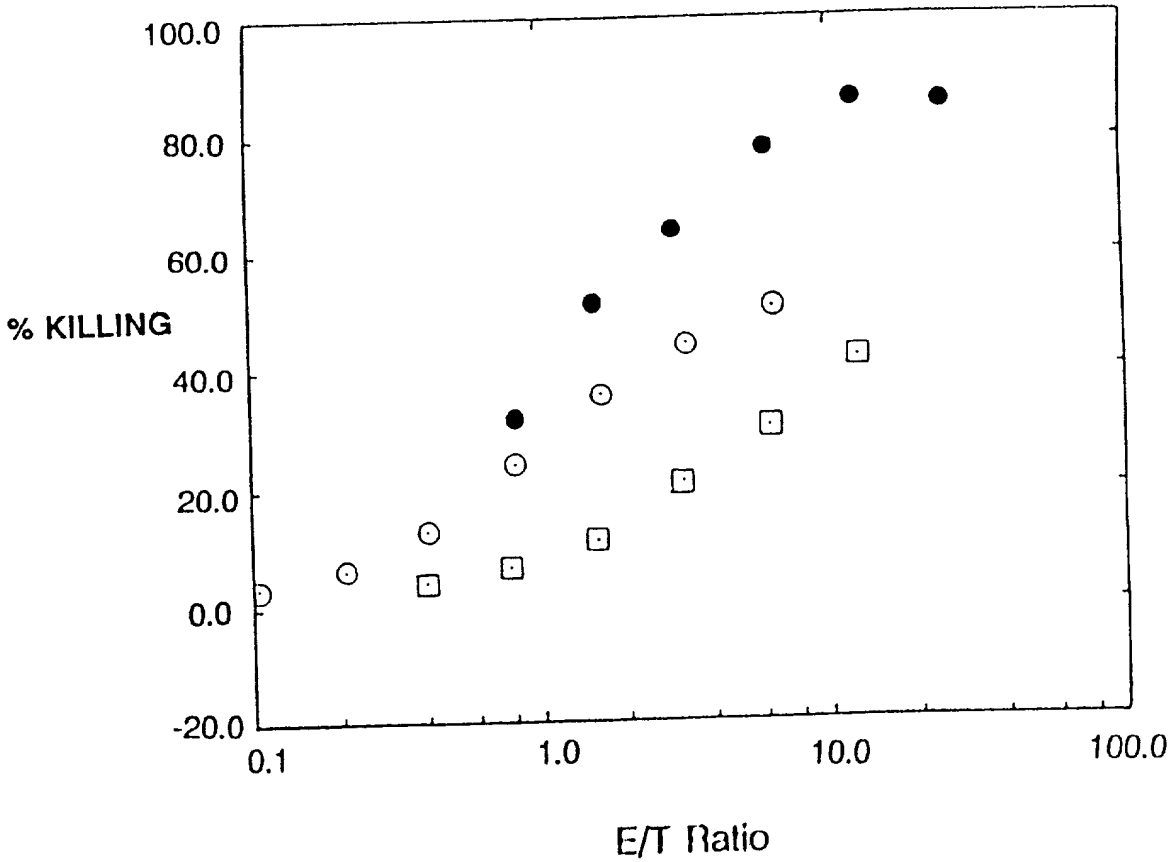

100.0
80.0
60.0
% KILLING
40.0
20.0
0.0
-20.0
0.1
1.0
10.0
100.0
E/T Ratio

FIG. 5c

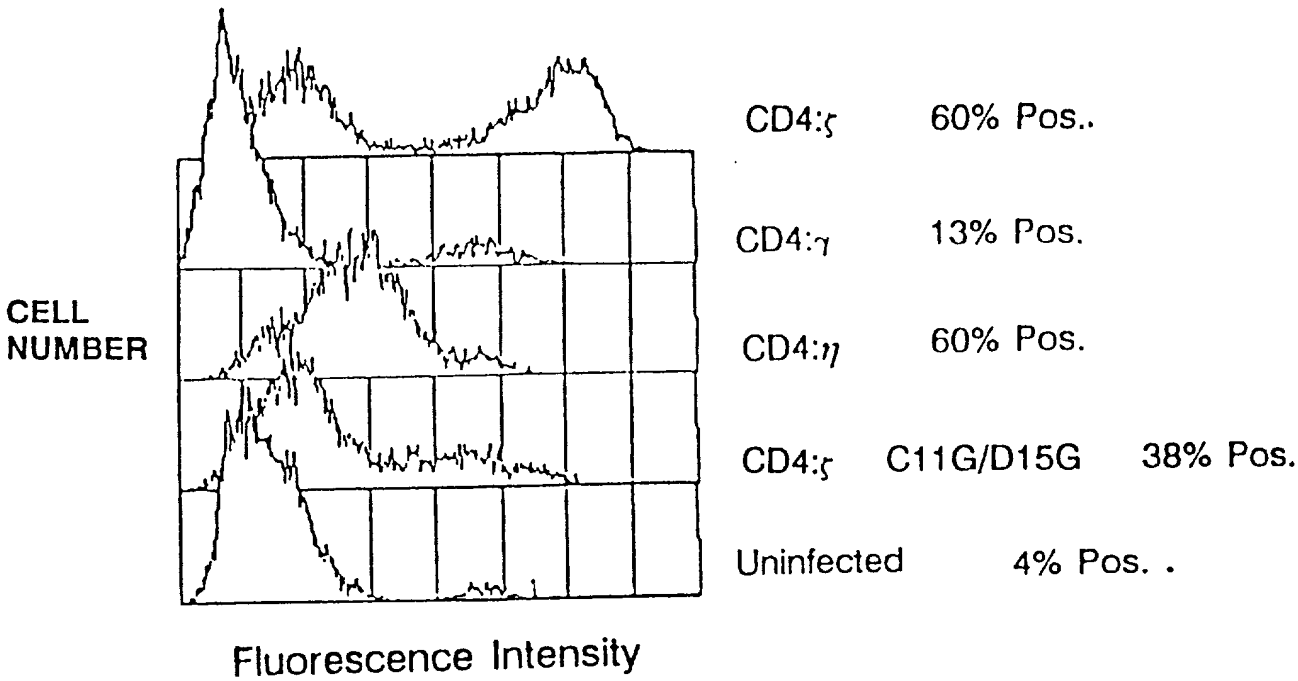

CELL
NUMBER
CD4:ζ 60% Pos..
CD4:γ 13% Pos.
CD4:η 60% Pos.
CD4:ζ C11G/D15G 38% Pos.
Uninfected 4% Pos. .
Fluorescence Intensity

FIG. 6a

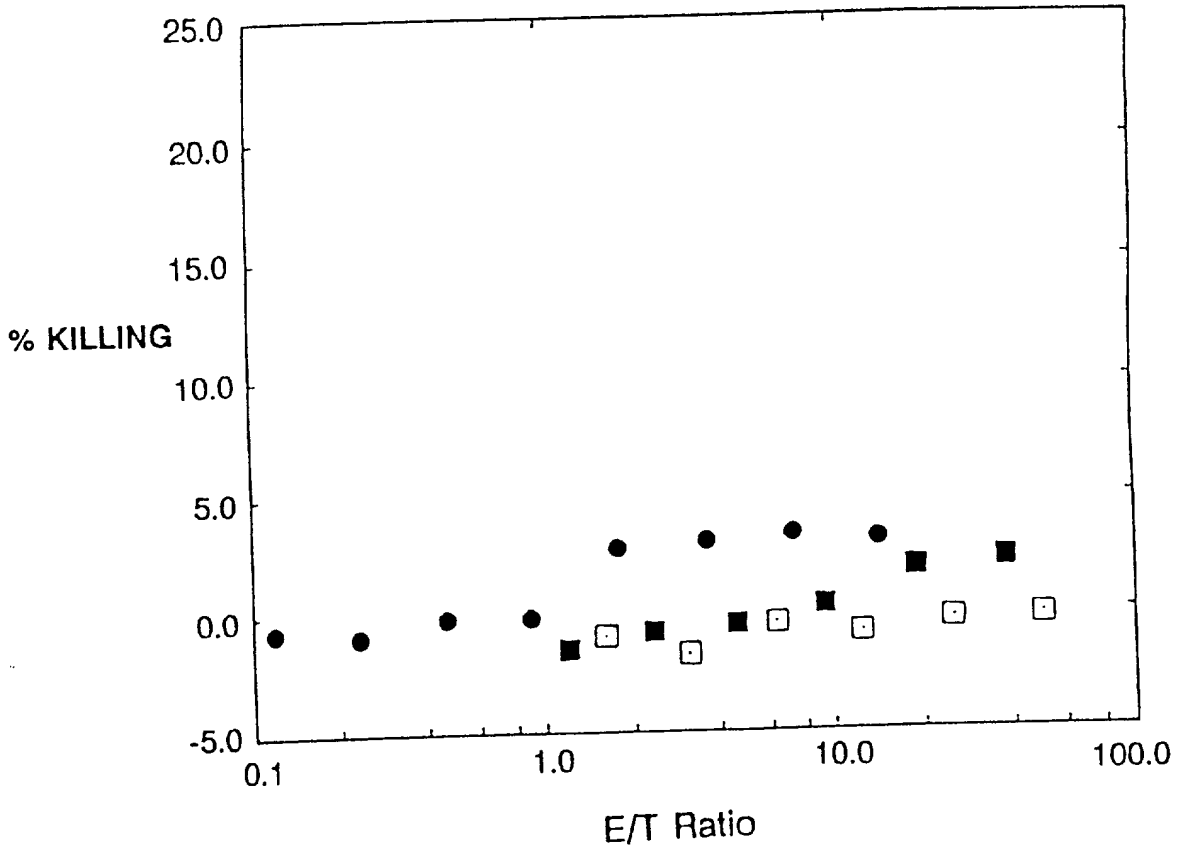

25.0
20.0
15.0
% KILLING
10.0
5.0
0.0
-5.0
0.1
1.0
10.0
100.0
E/T Ratio

FIG. 6b

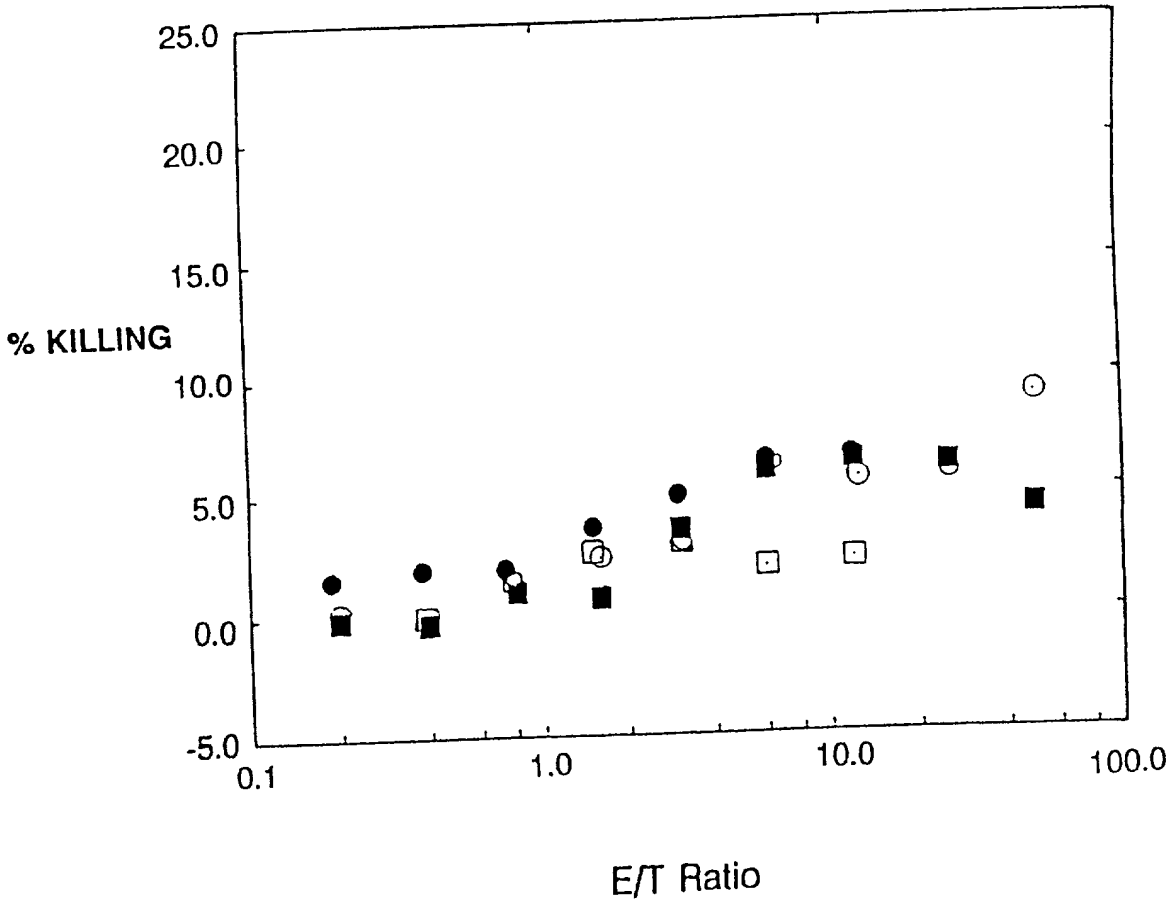

25.0
20.0
15.0
% KILLING
10.0
5.0
0.0
-5.0
0.1
1.0
10.0
100.0
E/T Ratio

FIG. 7a

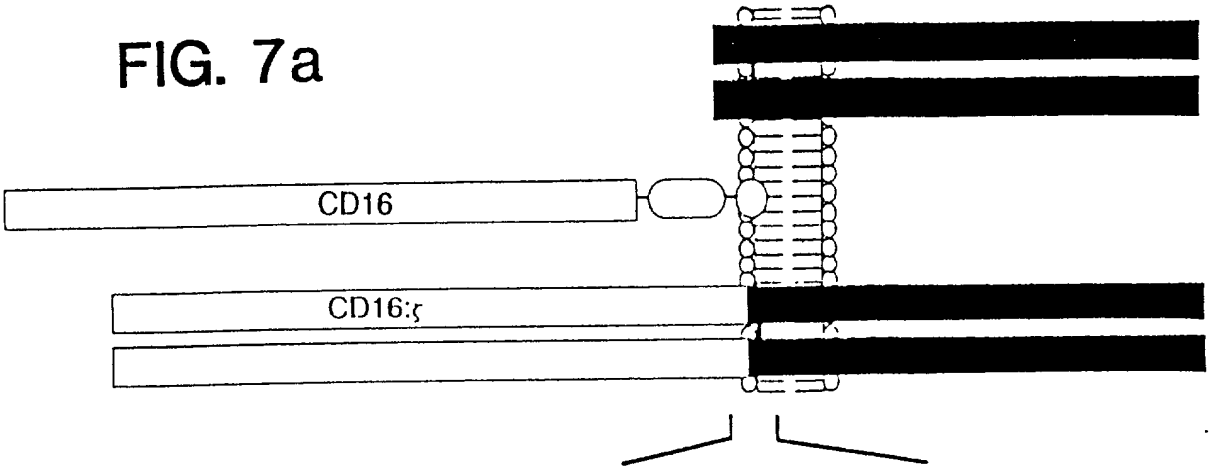

CD16
CD16:ζ
1
QSFGLLDPKLCYLLDG ζ
189
--FSPPGADPKLCYLLDG CD16:ζ

FIG. 7b

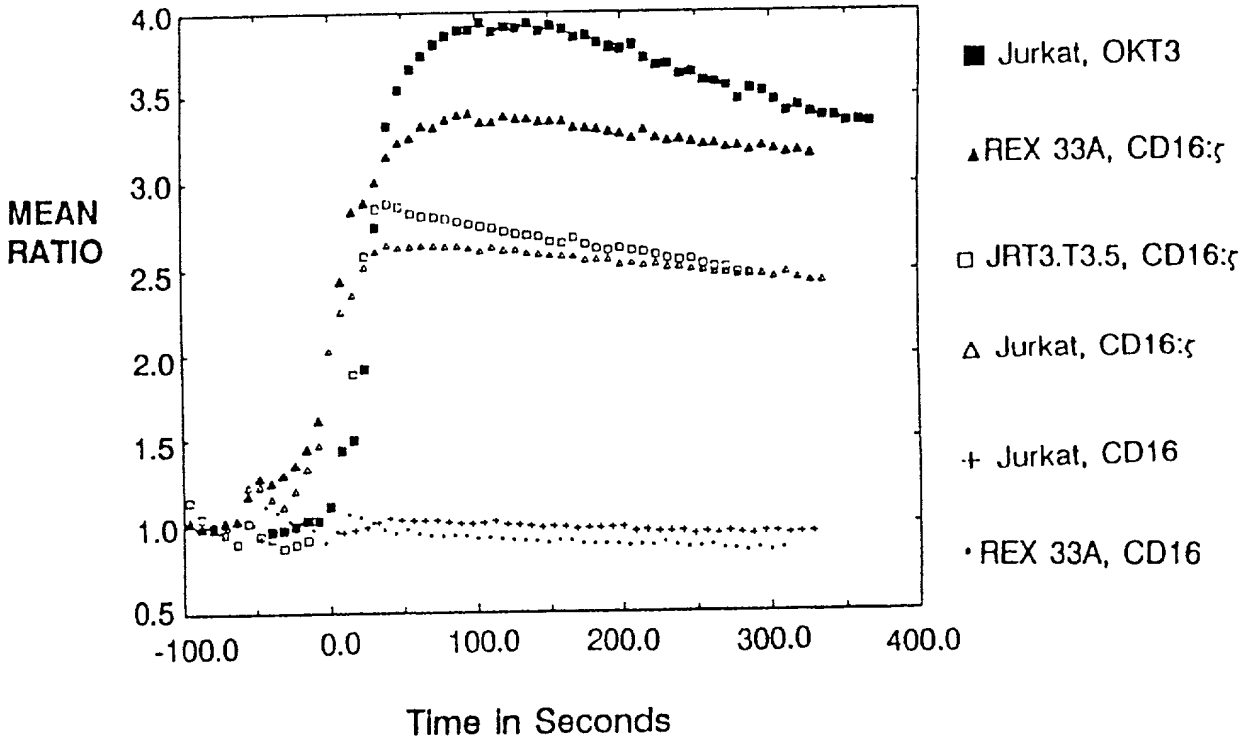

MEAN RATIO
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
-100.0
0.0
100.0
200.0
300.0
400.0
Time in Seconds
Jurkat, OKT3
REX 33A, CD16:ζ
JRT3.T3.5, CD16:ζ
Jurkat, CD16:ζ
Jurkat, CD16
REX 33A, CD16

FIG. 8a

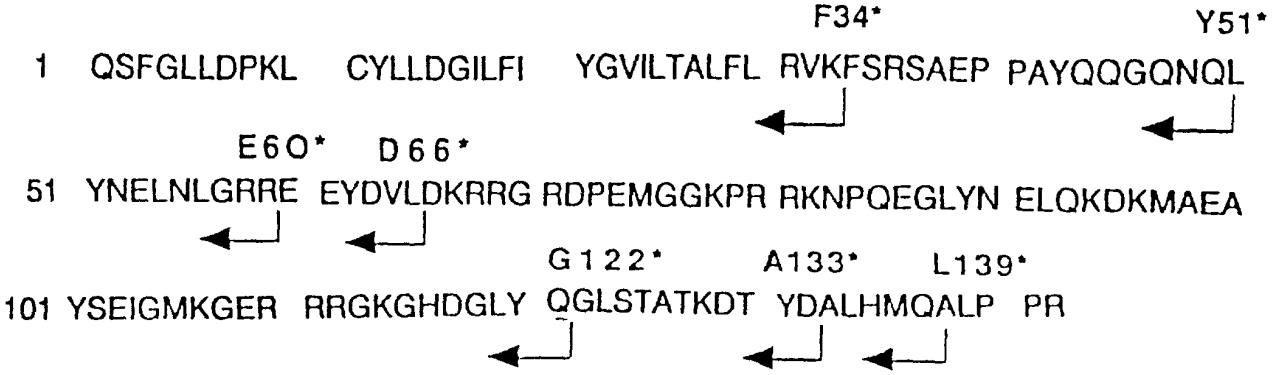

F34*
Y51*
1 QSFGLLDPKL CYLLDGILFI YGVILTALFL RVKFSRSAEP PAYQQGQNQL
E60* D66*
51 YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA
G122* A133* L139*
101 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

FIG. 8b

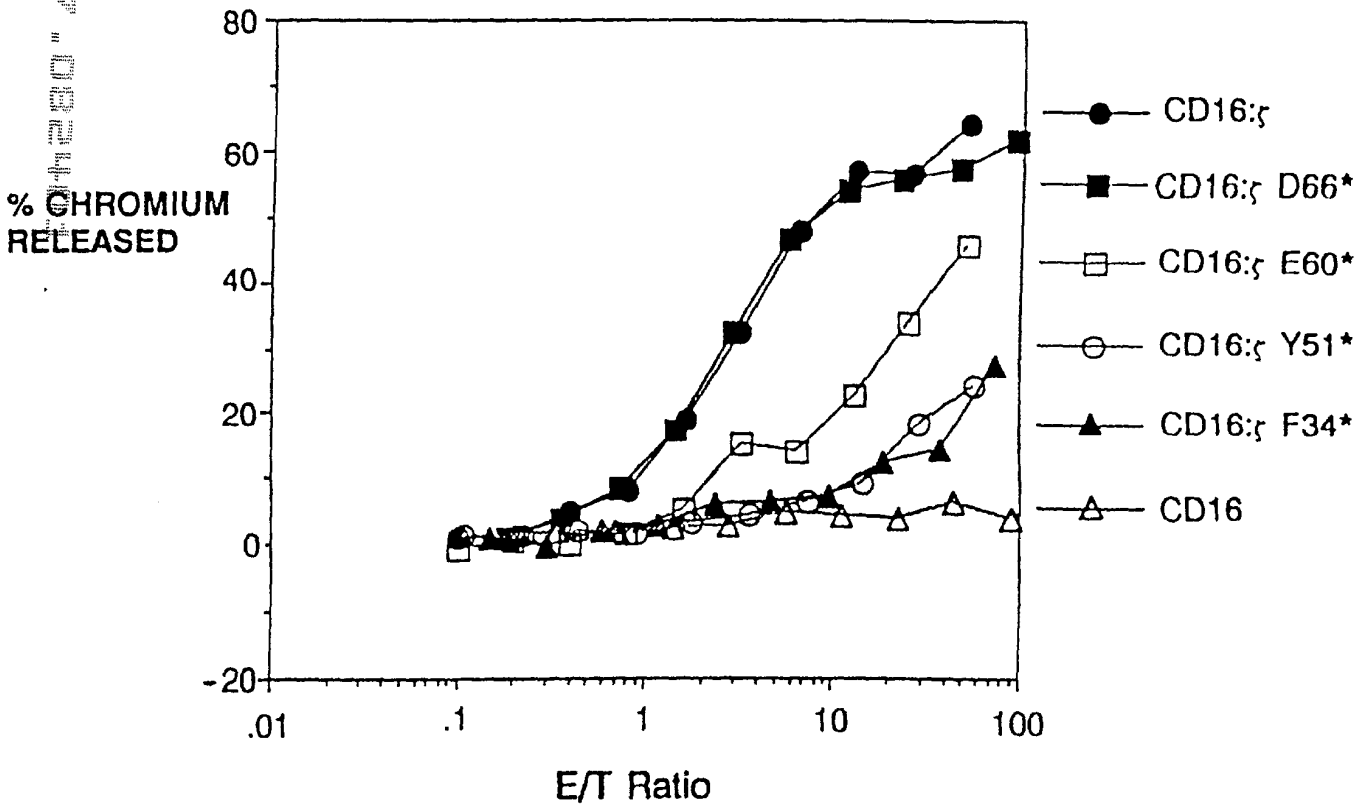

% CHROMIUM RELEASED
80
60
40
20
0
-20
.01
.1
1
10
100
E/T Ratio
CD16:ζ
CD16:ζ D66*
CD16:ζ E60*
CD16:ζ Y51*
CD16:ζ F34*
CD16

FIG. 9a

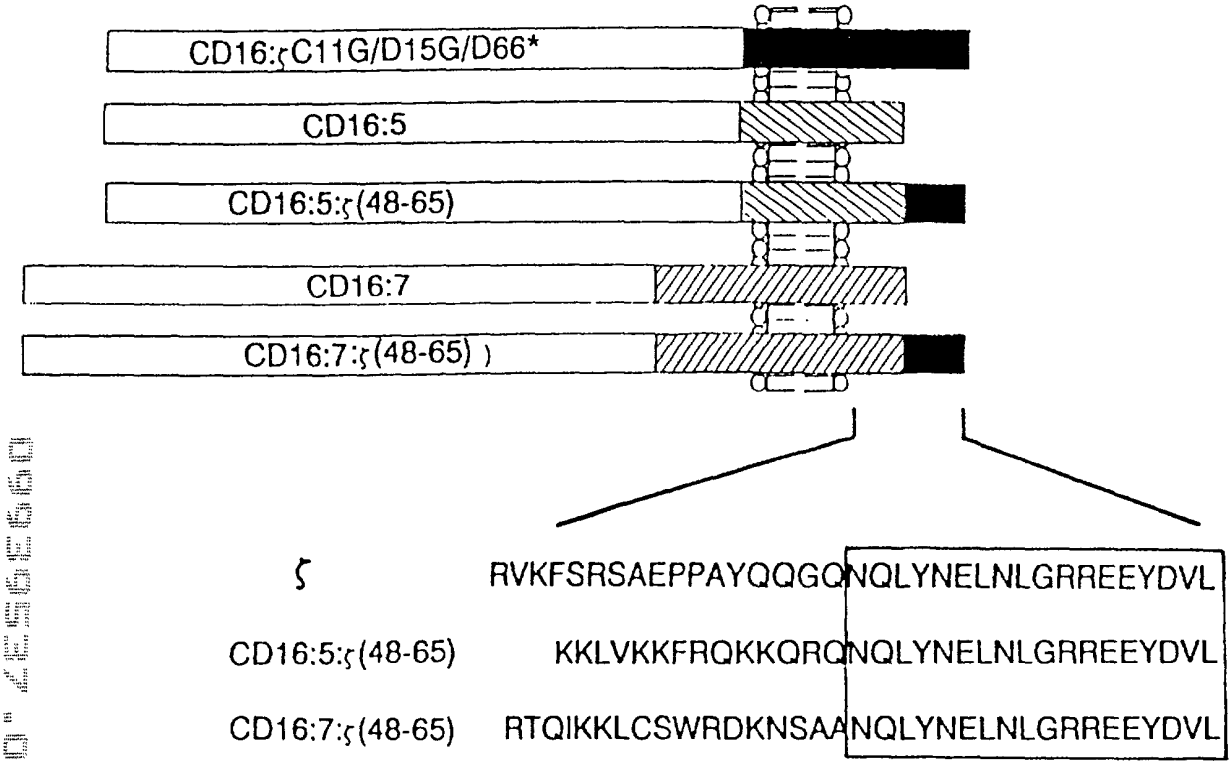

CD16:ζC11G/D15G/D66*
CD16:5
CD16:5:ζ(48-65)
CD16:7
CD16:7:ζ(48-65))
ζ RVKFSRSAEPPAYQQGQNQLYNELNLGRREEYDVL
CD16:5:ζ(48-65) KKLVKKFRQKKQRQNQLYNELNLGRREEYDVL
CD16:7:ζ(48-65) RTQIKKLCSWRDKNSAANQLYNELNLGRREEYDVL

FIG. 9b

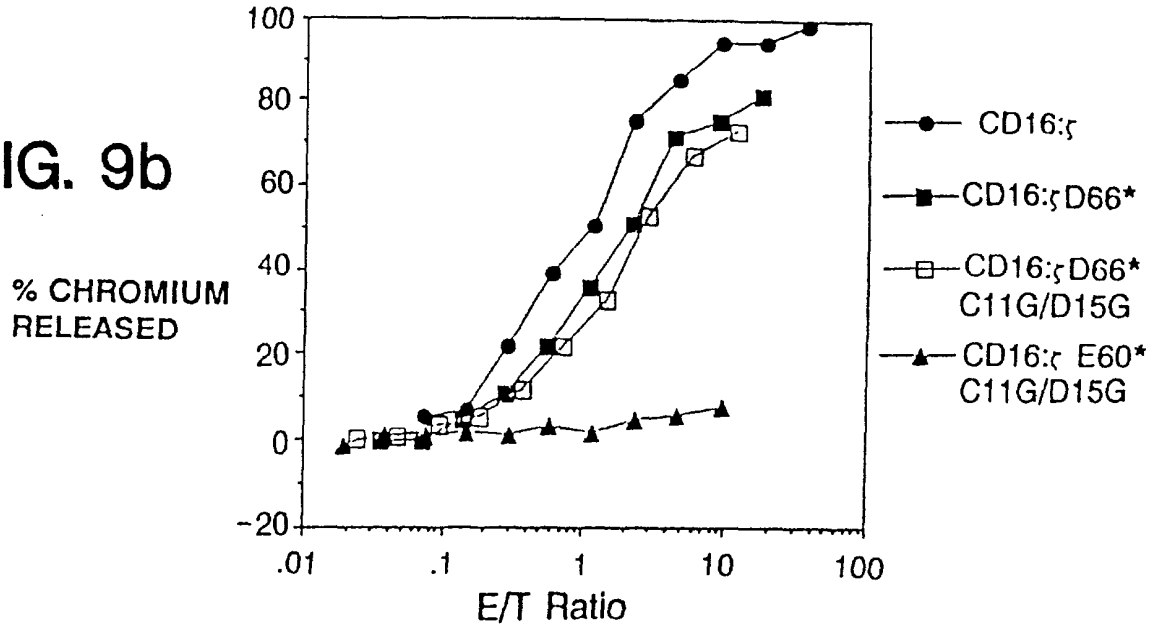

% CHROMIUM RELEASED
100
80
60
40
20
0
-20
.01
.1
1
10
100
E/T Ratio
CD16:ζ
CD16:ζD66*
CD16:ζD66* C11G/D15G
CD16:ζ E60* C11G/D15G

FIG. 9c

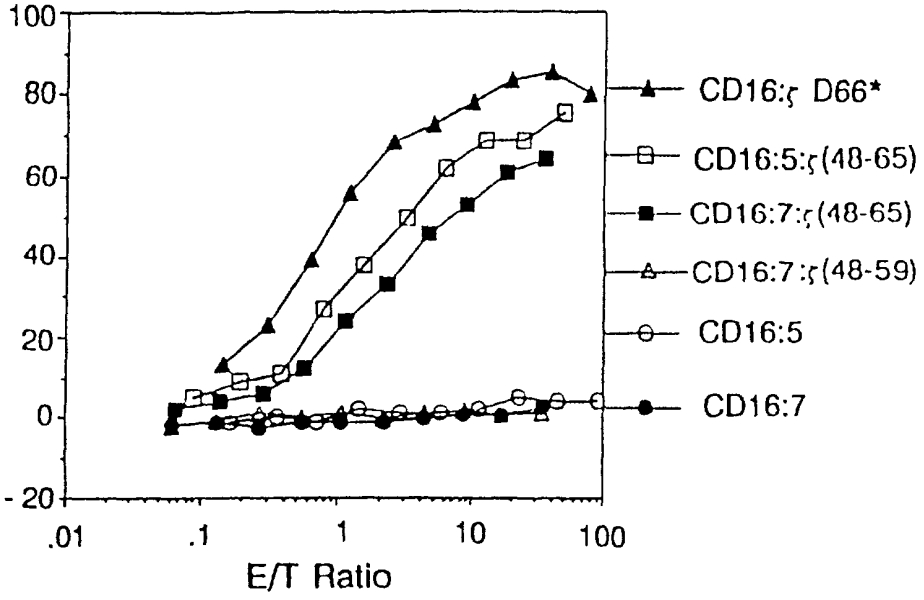

100
80
60
40
20
0
- 20
.01
.1
1
10
100
E/T Ratio
CD16:ζ D66*
CD16:5:ζ(48-65)
CD16:7:ζ(48-65)
CD16:7:ζ(48-59)
CD16:5
CD16:7

FIG. 9d

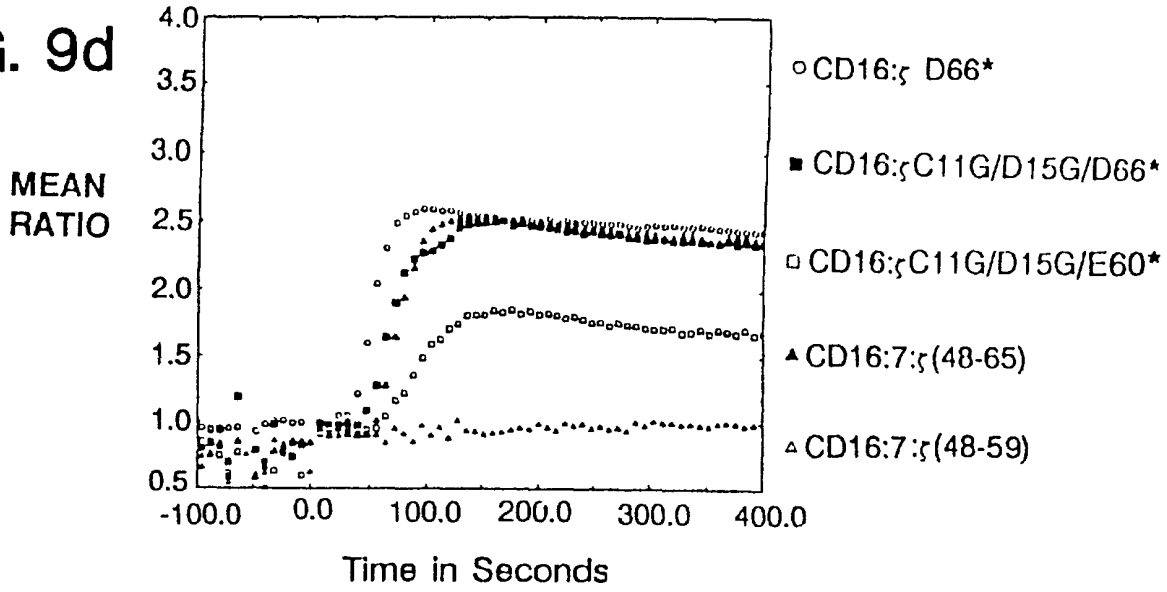

MEAN RATIO
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
-100.0
0.0
100.0
200.0
300.0
400.0
Time in Seconds
CD16:ζ D66*
CD16:ζC11G/D15G/D66*
CD16:ζC11G/D15G/E60*
CD16:7:ζ(48-65)
CD16:7:ζ(48-59)

FIG. 10a

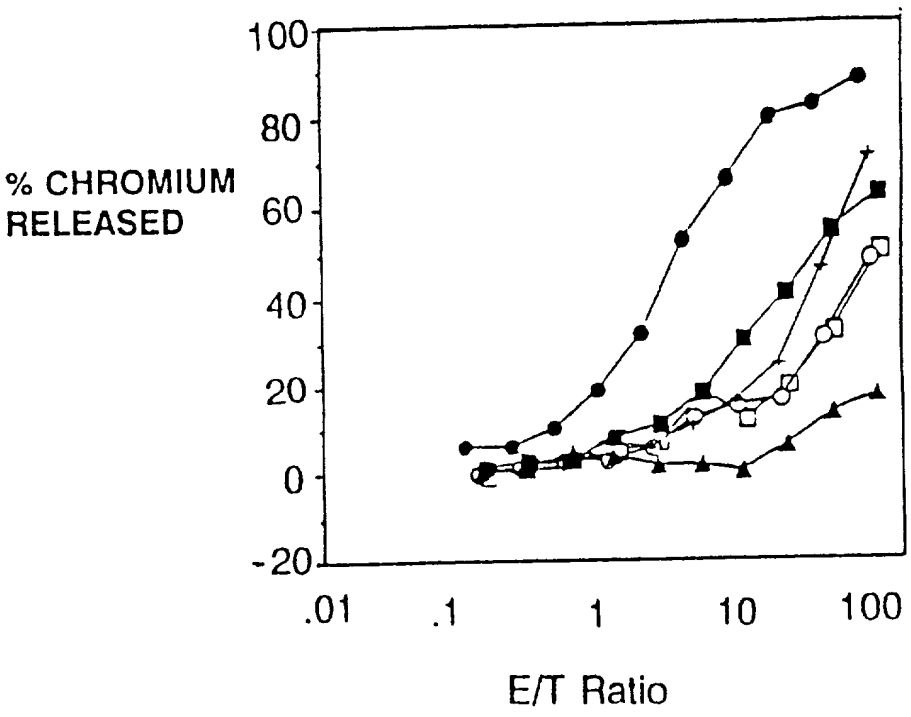


FIG. 10b

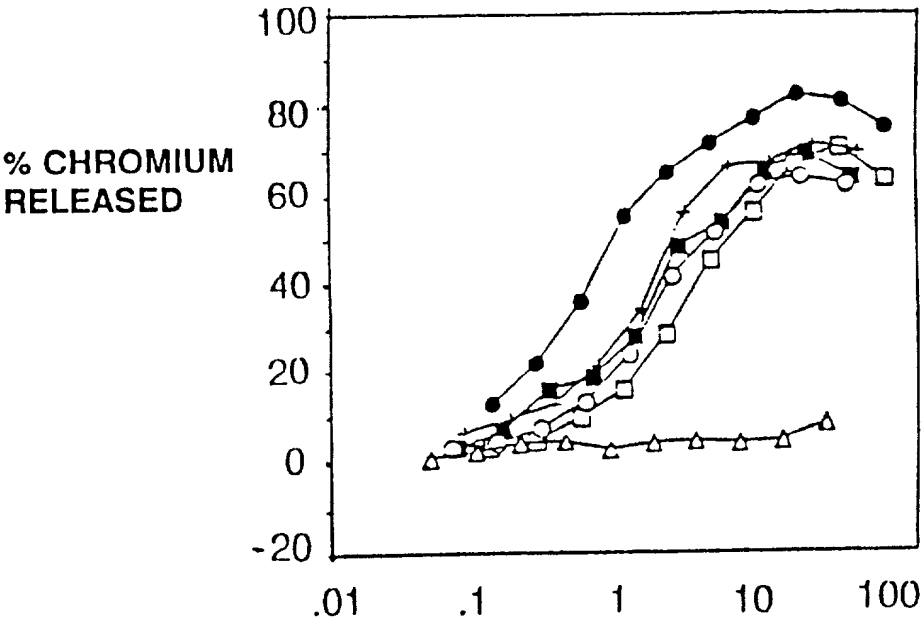


FIG. 10c

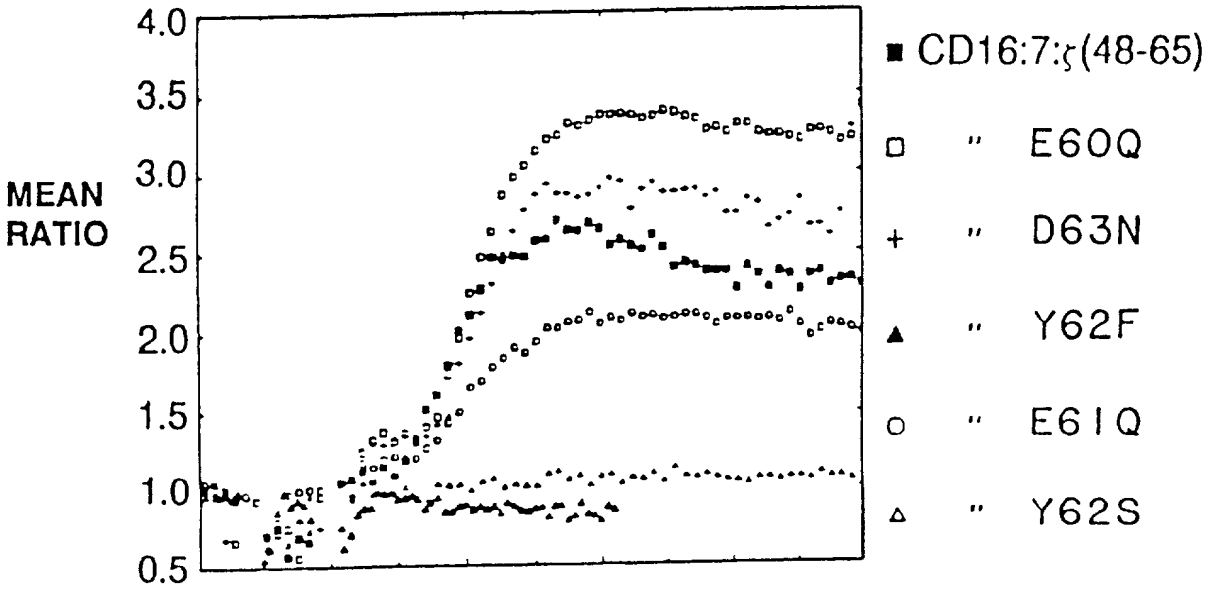


FIG. 10d

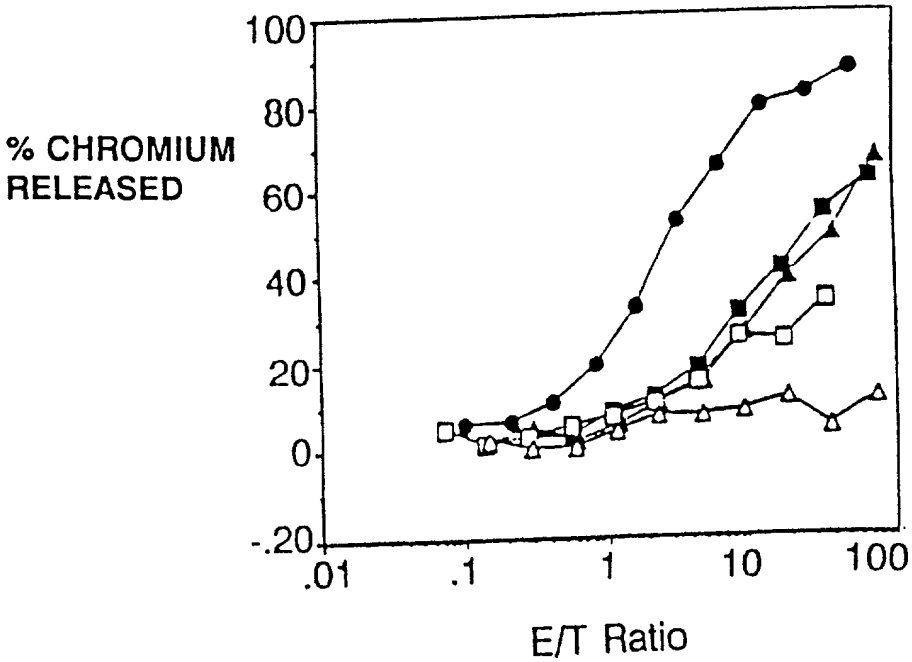


FIG. 10e

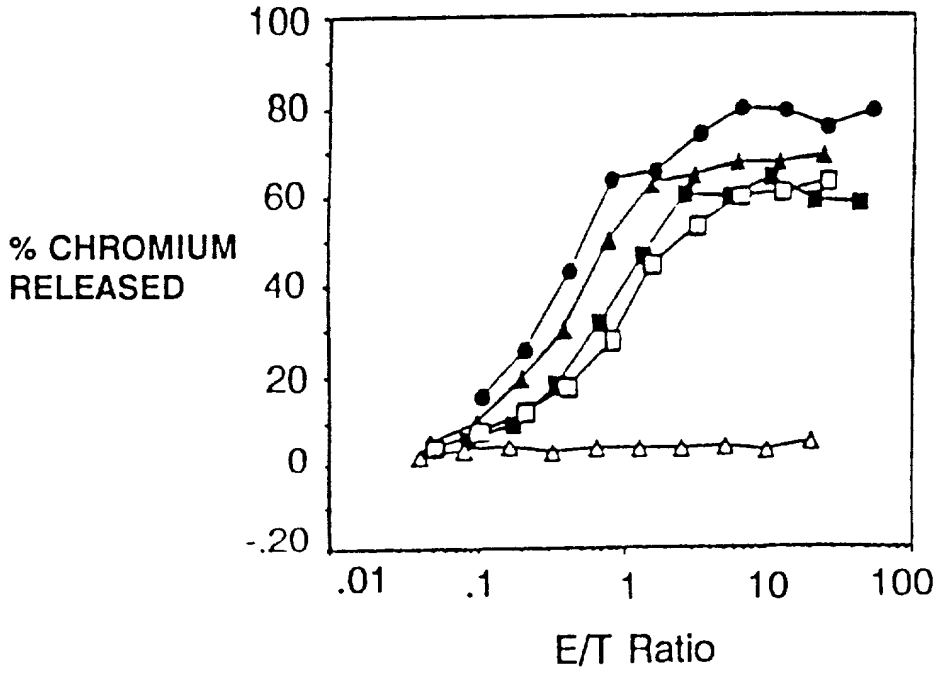


FIG. 10f

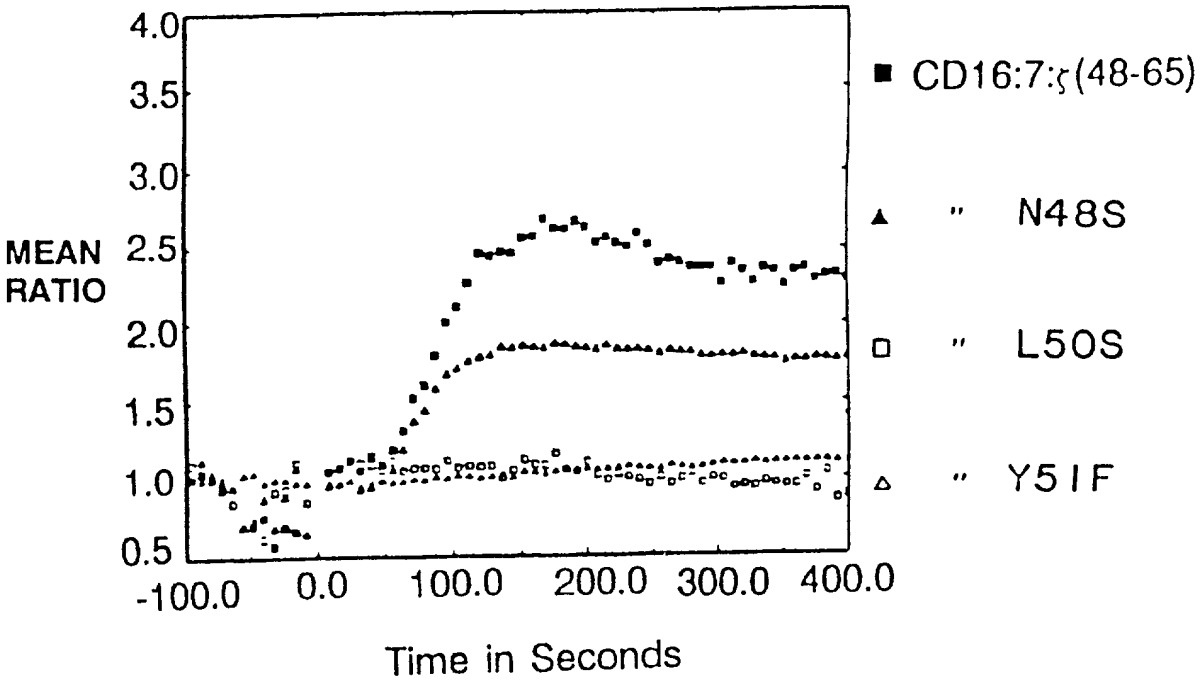


FIG. 11a

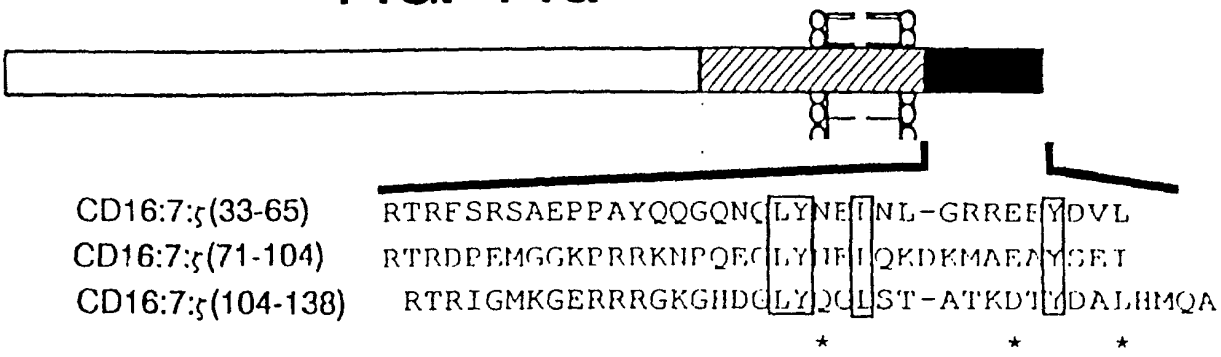
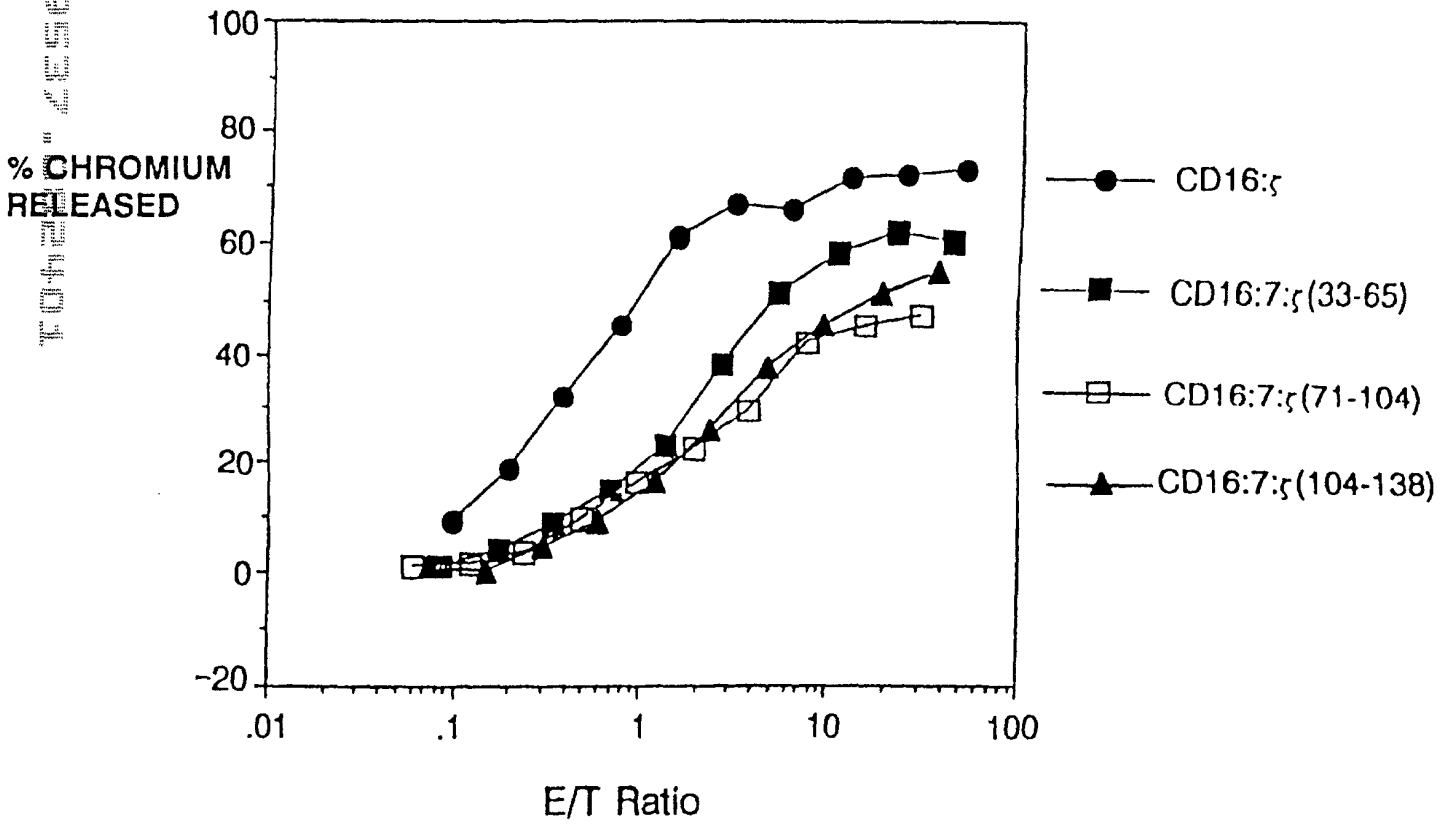


FIG. 11b



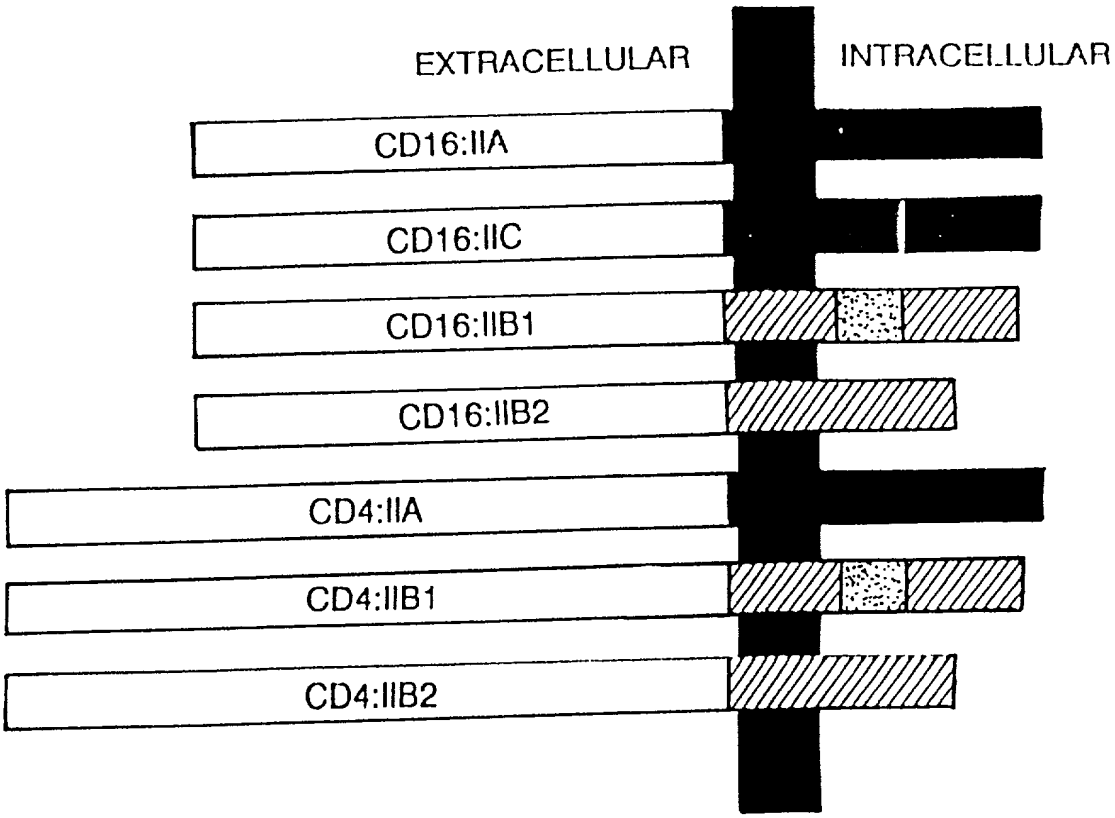

EXTRACELLULAR
INTRACELLULAR
CD16:IIA
CD16:IIC
CD16:IIB1
CD16:IIB2
CD4:IIA
CD4:IIB1
CD4:IIB2

FIG. 12

FIG. 13a

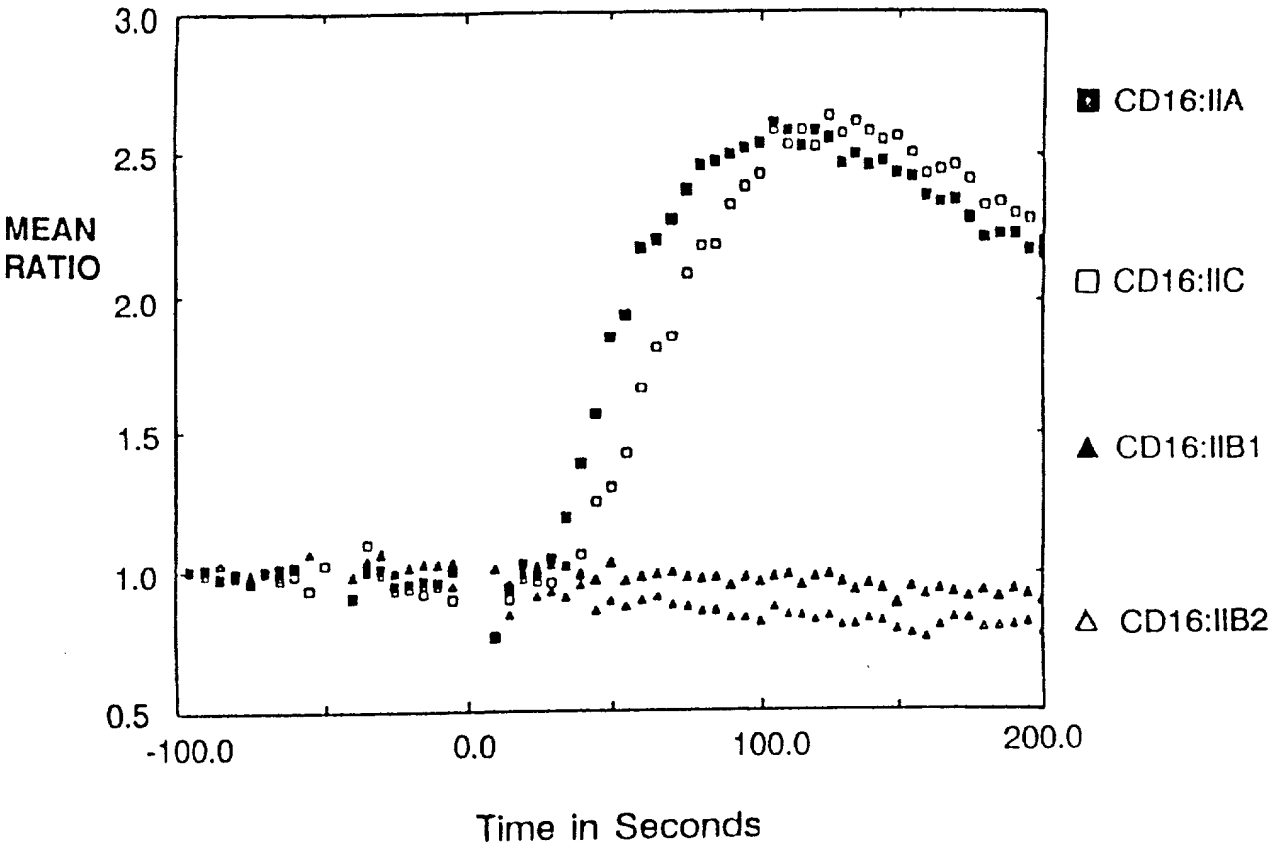


FIG. 13b

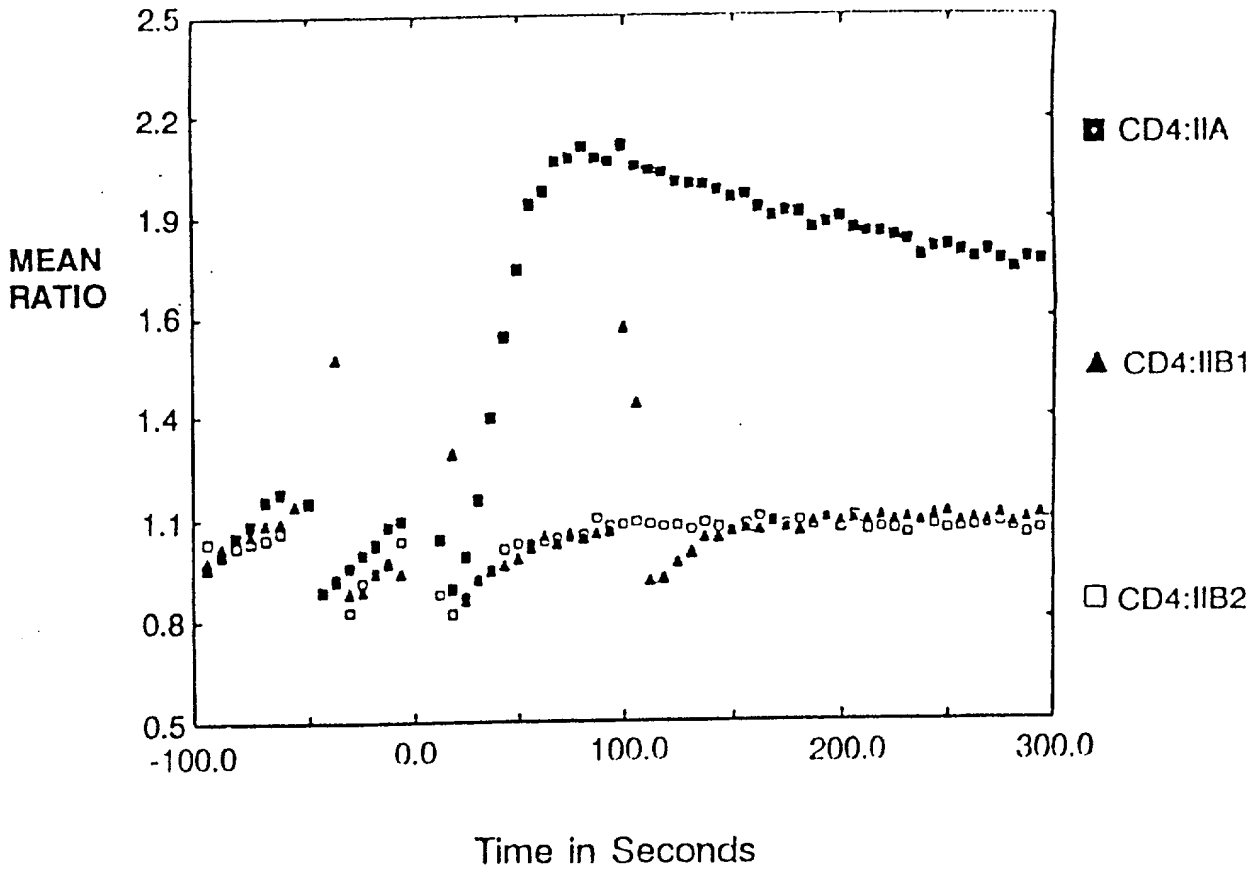


FIG. 14a

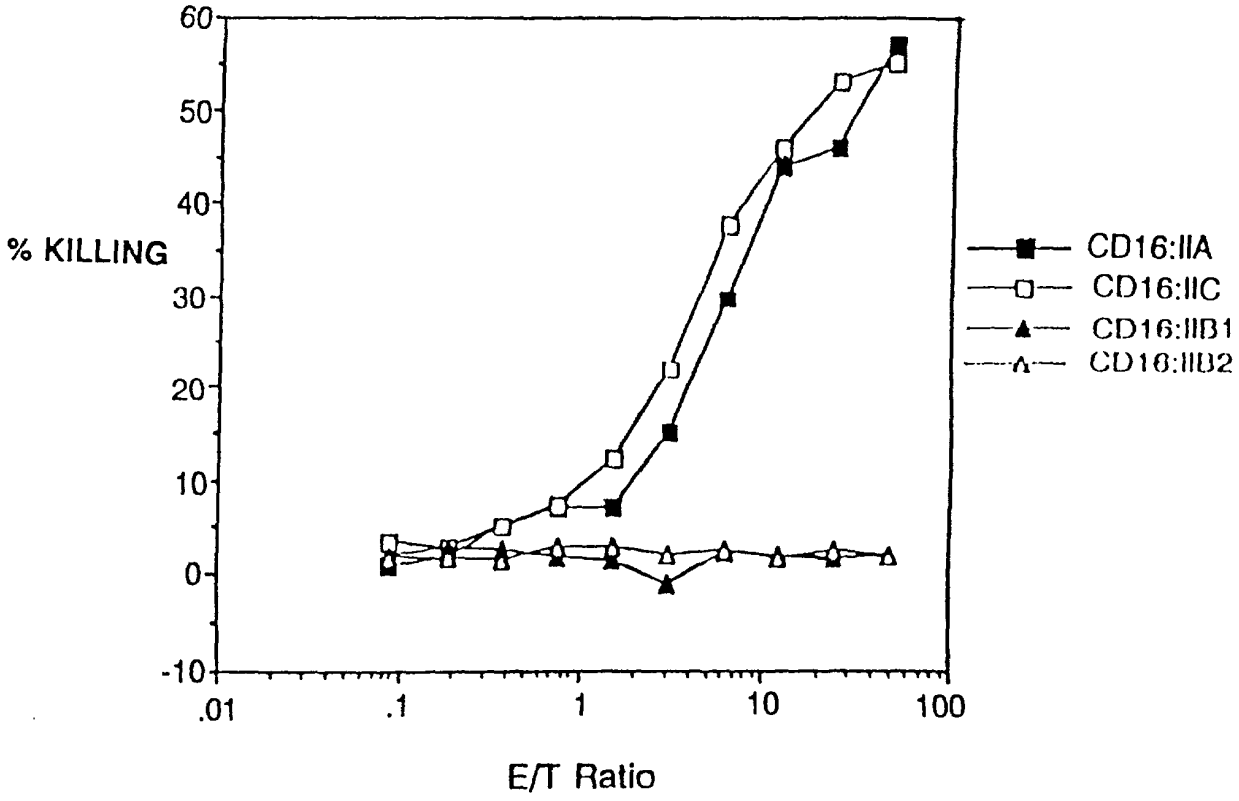


FIG. 14b

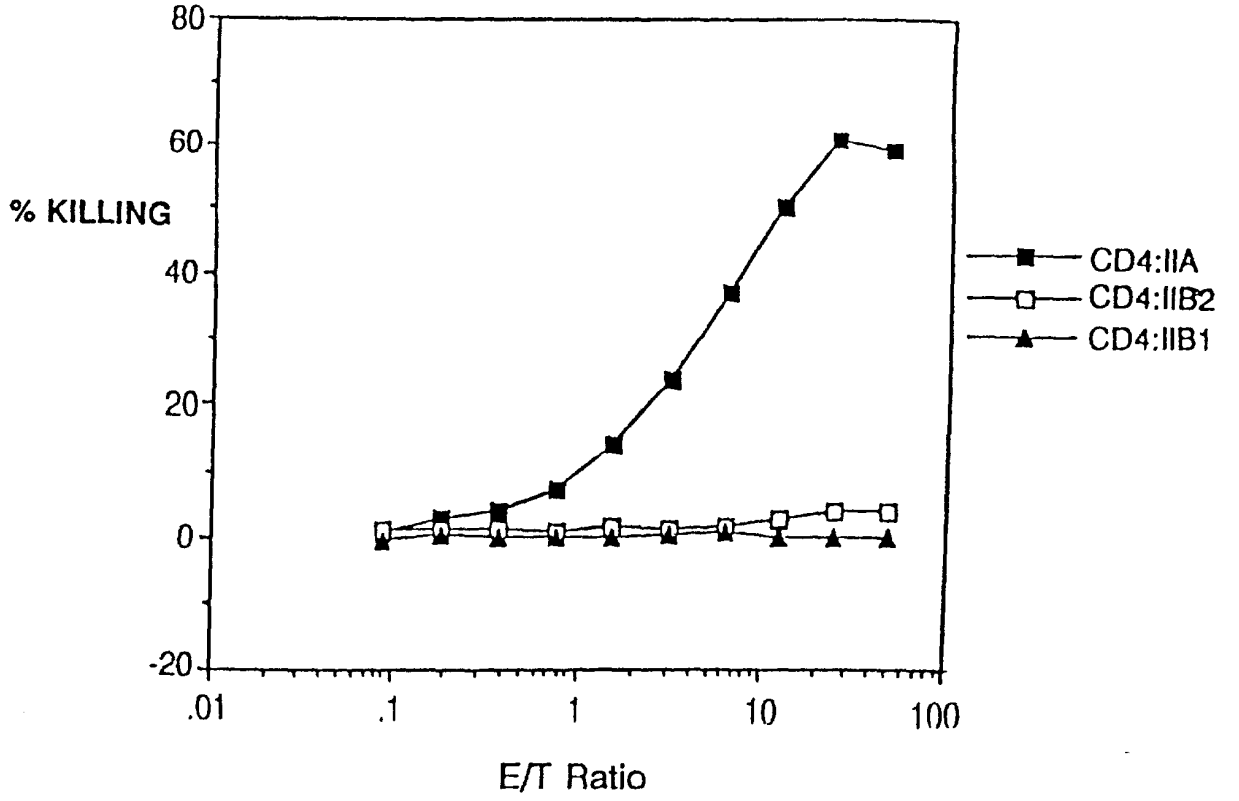


FIG. 15a

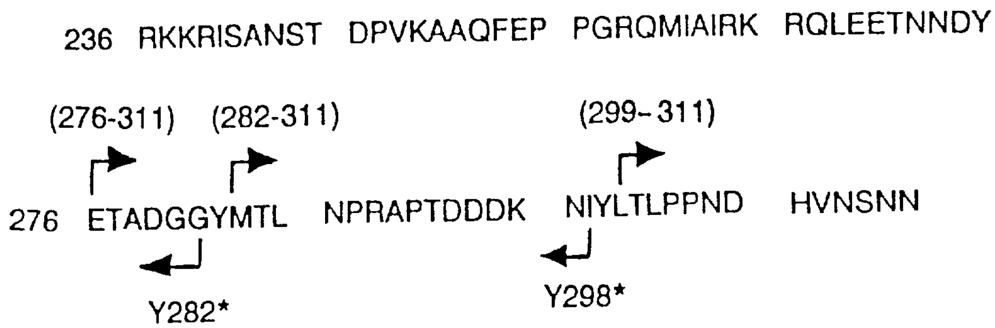


FIG. 15b

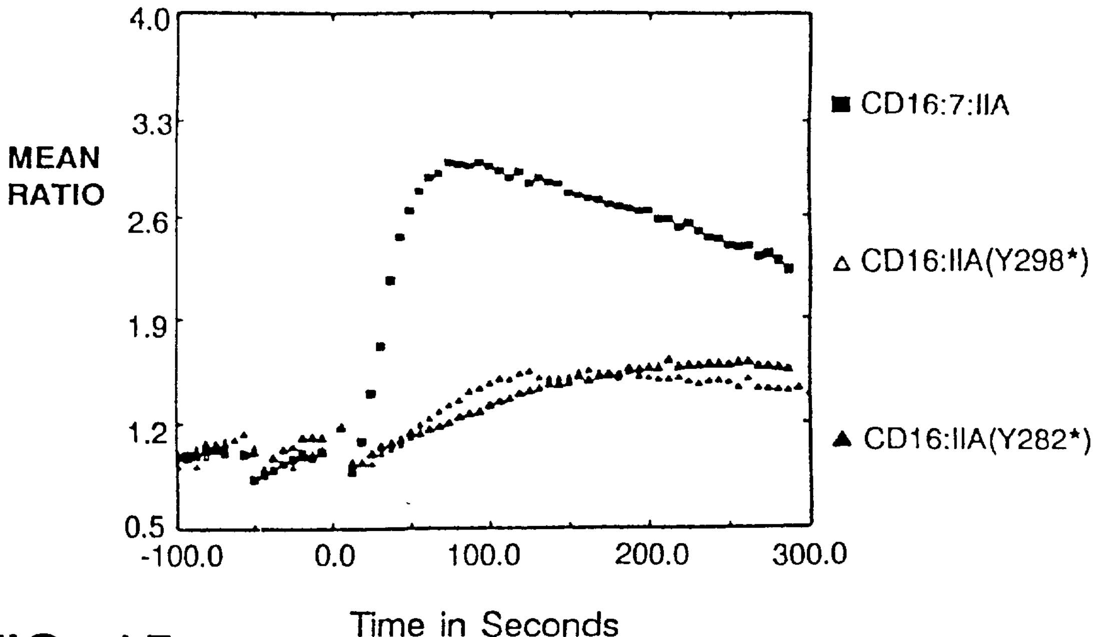


FIG. 15c

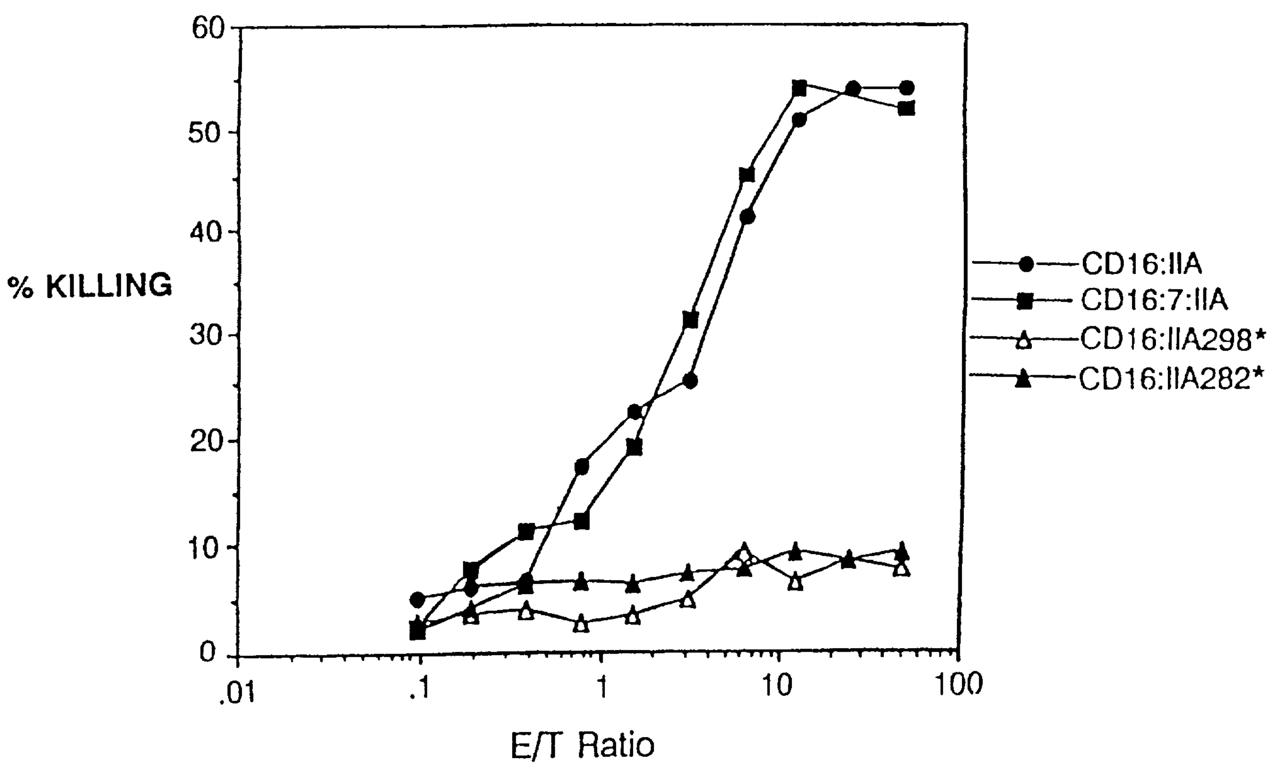


FIG. 15d

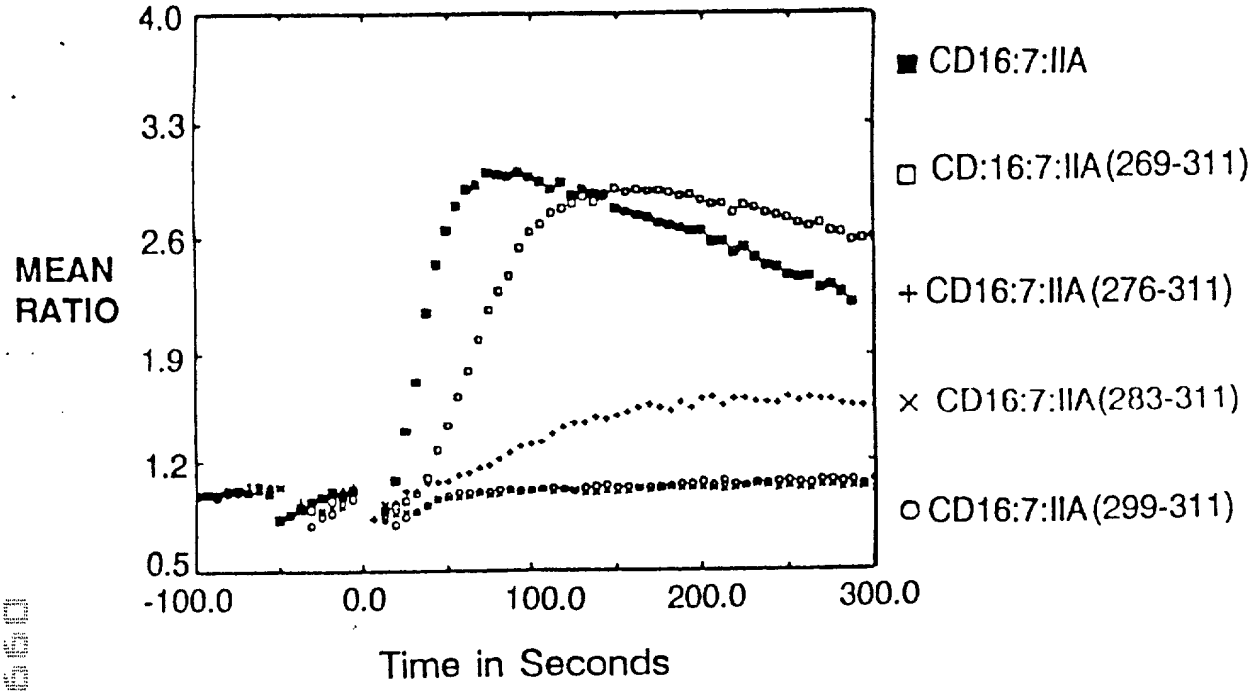


FIG. 15e

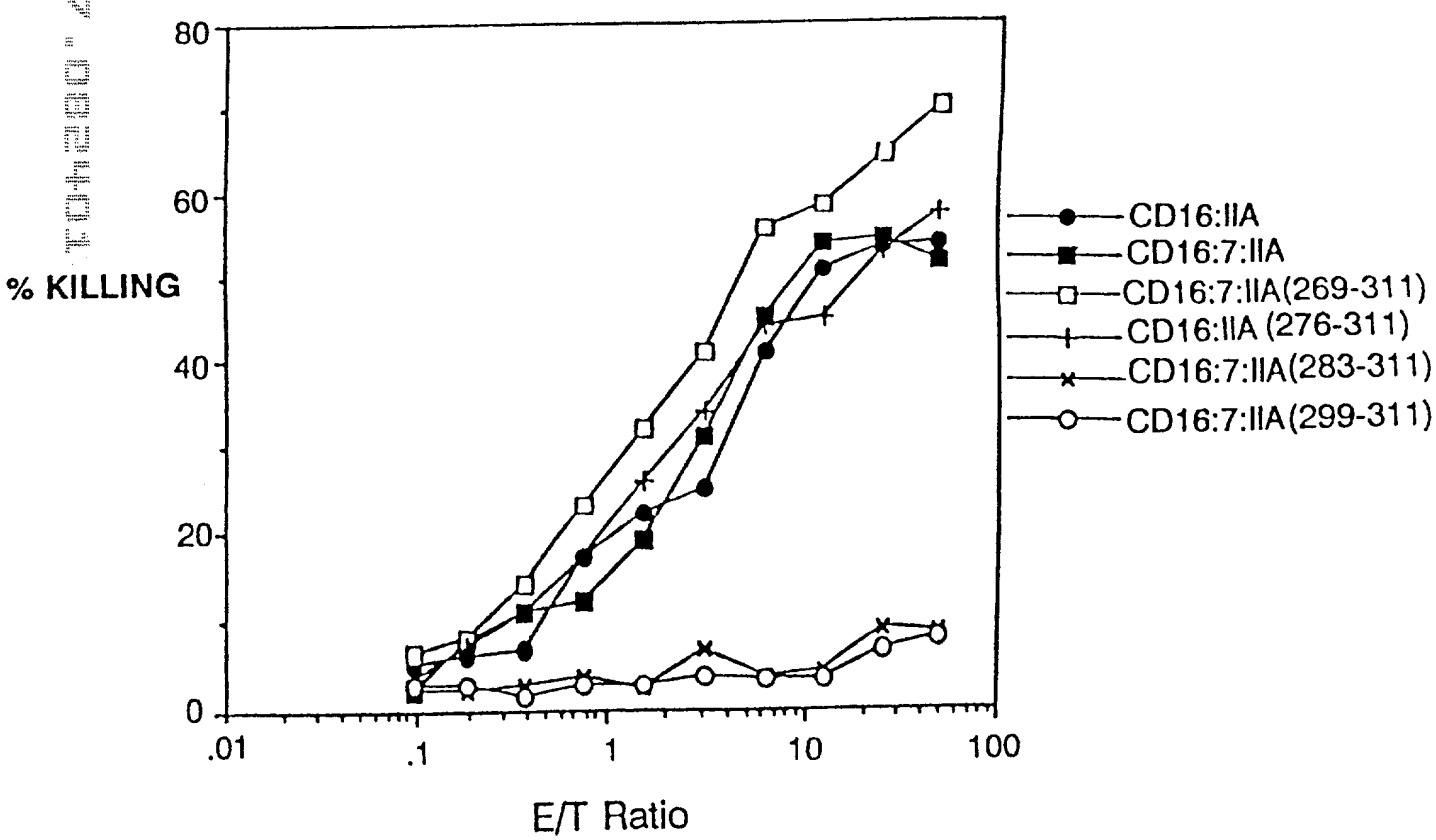


FIG.16 (Seq. ID No: 24)

1 MEHSTFLSGL VLATLLSQVS PFKIPIEELE DRVFVNCNTS ITWVEGTVGT

51 LLSDITRLDL GKRILDPRGI YRCNGTDIYK DKESTVQVHY RMCQSCVELD

101 PATVAGIIVT DVIATLLLAL GVFCFAGHET GRLSGAADTQ ALLRNDQVYQ

151 PLRDRDDAQY SHLGGNWARN K*

FIG.17 (Seq ID NO: 25)

1 MEQGKGLAVL ILAIILLQGT LAQSIKGNHL VKVYDYQEDG SVLLTCDAEA

51 KNITWFKDGK MIGFLTEDKK KWNLGSNAKD PRGMYQCKGS QNKSKPLQVY

101 YRMCQNCIEL NAATISGFLF AEIVSIFVLA VGVYFIAGQD GVRQSRASDK

151 QTLLPNDQLY QPLKDREDDQ YSHLQGNQLR RN*

FIG.18 (Seq ID No: 26)

1 MPGGLEALRA LPLLLFLSYA CLGPGCQALR VEGGPPSLTV NLGEEARLTC

51 ENNGRNPNIT WWFSLQSNIT WPPVPLGPGQ GTTGQLFFPE VNKNTGACTG

101 CQVIENNILK RSCGTYLRVR NPVPRPFLDM GEGTKNRIIT AEGIILLFCA

151 VVPGTLLLFR KRWQNEKFGV DMPDDYEDEN LYEGLNLDDC SMYEDISRGL

201 QGTYQDVGNL HIGDAQLEKP *

FIG.19 (Seq ID No: 27)

1 MATLVLSSMP CHWLLFLLLL FSGEPVPAMT SSDLPLNFQG SPCSQIWQHP

51 RFAAKKRSSM VKFHCYTNHS GALTWFRKRG SQQPQELVSE EGRIVQTQNG

101 SVYTLTIQNI QYEDNGIYFC KQKCDSANHN VTDSCGTELL VLGFSTLDQL

151 KRRNTLKDGI ILIQTLLIIL FIIVPIFLLL DKDDGKAGME EDHTYEGLNI

201 DQTATYEDIV TLRTGEVKWS VGEHPGQE*

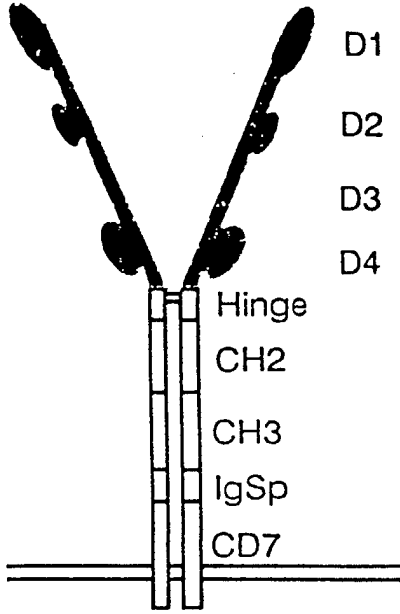


FIG. 20a

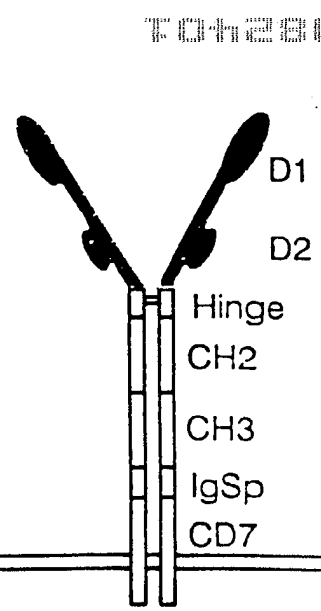


FIG. 20b

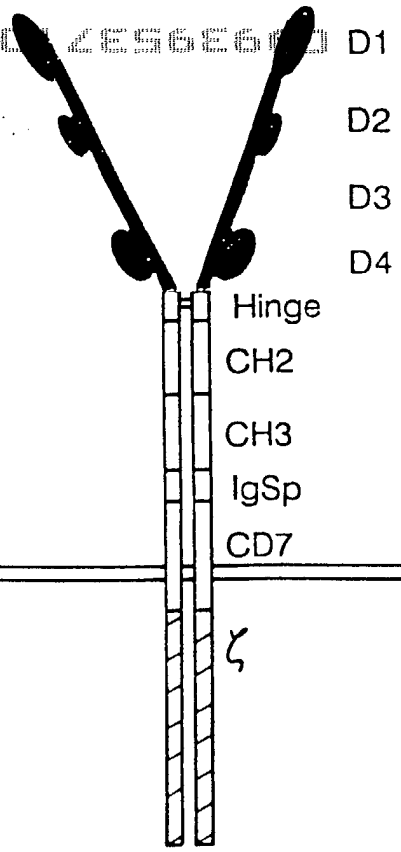


FIG.20c

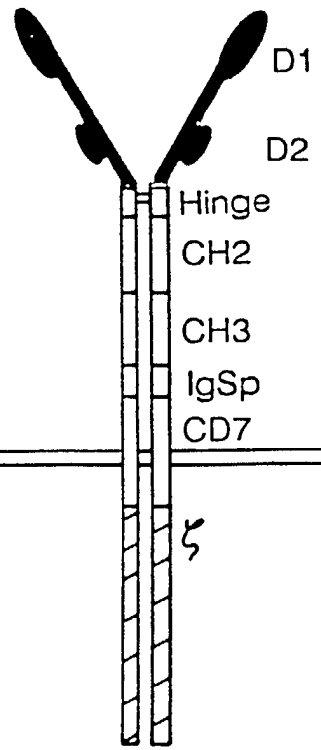


FIG. 20d

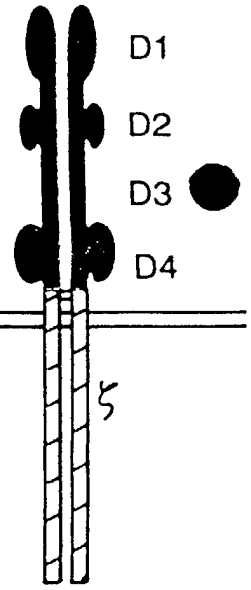


FIG. 20e

BamHI/BstY1 Bgl2/BstY1

G GAT CCC AAG GCC AGG CTA AAG CCG AAG CCG CGA AGG CCG AGG CTA AGG CCG AAG CAG ATC TG

D P K A E A K A E A K A E A K A E A D L

FIG. 28

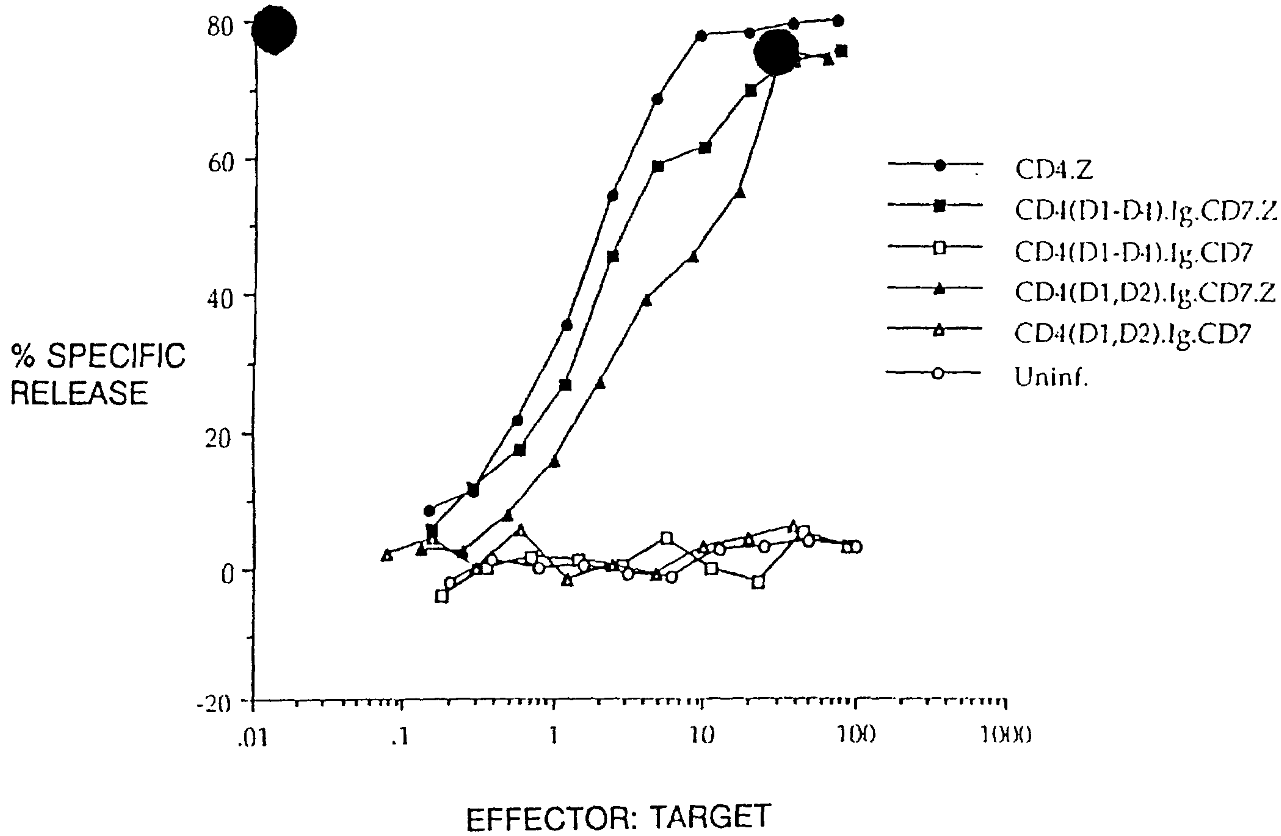


FIG. 21

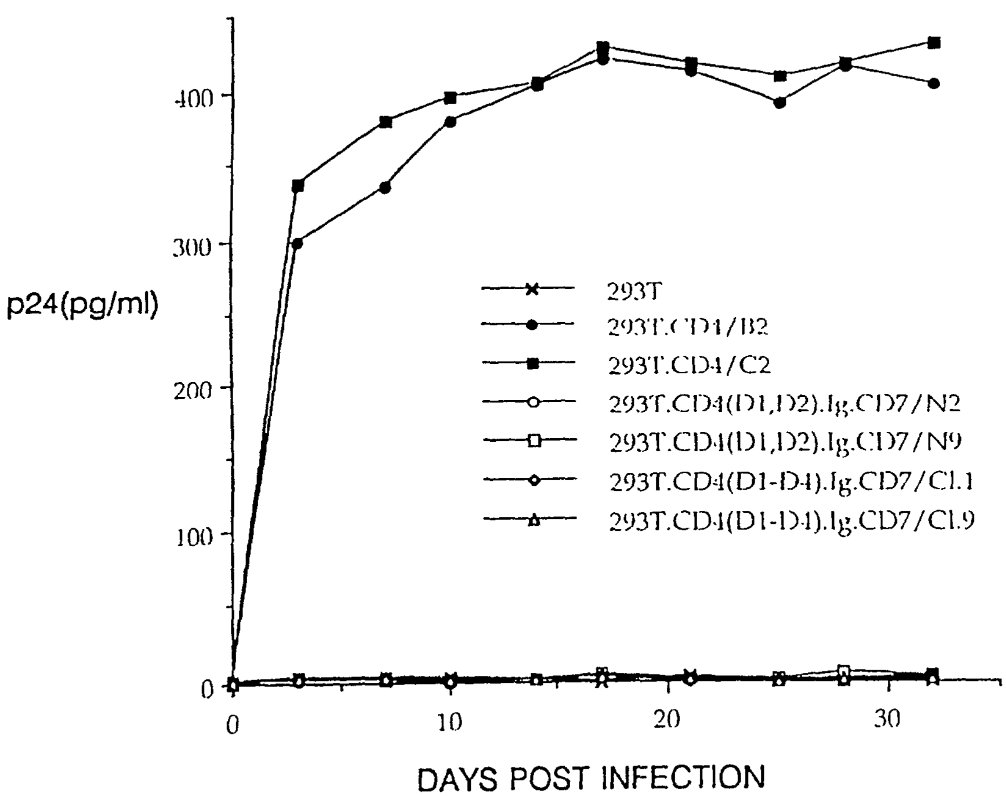


FIG. 22

D1-D4 of CD4

Nucleic Acid Sequence

```
GCCTGTTTGA GAAGCAGCGG GCAAGAAAGA CGCAAGCCCA GAGGCCCTGC          51
CATTTCTGTG GGCTCAGGTC CCTACTGGCT CAGGCCCCTG CCTCCCTCGG         101
CAAGGCCACA ATGAACCGGG GAGTCCCTTT TAGGCACTTG CTTCTGGTGC         151
TGCAACTGGC GCTCCTCCCA GCAGCCACTC AGGGAAACAA AGTGGTGCTG         201
GGCAAAAAAG GGGATACAGT GGAACTGACC TGTACAGCTT CCCAGAAGAA         251
GAGCATACAA TTCCACTGGA AAAACTCCAA CCAGATAAAG ATTCTGGGAA         301
ATCAGGGCTC CTTCTTAACT AAAGGTCCAT CCAAGCTGAA TGATCGCGCT         351
GACTCAAGAA GAAGCCTTTG GGACCAAGGA AACTTCCCCC TGATCATCAA         401
GAATCTTAAG ATAGAAGACT CAGATACTTA CATCTGTGAA GTGGAGGACC         451
AGAAGGAGGA GGTGCAATTG CTAGTGTTCG GATTGACTGC CAACTCTGAC         501
ACCCACCTGC TTCAGGGGCA GAGCCTGACC CTGACCTTGG AGAGCCCCCC         551
TGGTAGTAGC CCCTCAGTGC AATGTAGGAG TCCAAGGGGT AAAAACATAC         601
AGGGGGGGAA GACCCTCTCC GTGTCTCAGC TGGAGCTCCA GGATAGTGGC         651
ACCTGGACAT GCACTGTCTT GCAGAACCAG AAGAAGGTGG AGTTCAAAAT         701
AGACATCGTG GTGCTAGCTT TCCAGAAGGC CTCCAGCATA GTCTATAAGA         751
AAGAGGGGGA ACAGGTGGAG TTCTCCTTCC CACTCGCCTT TACAGTTGAA         801
AAGCTGACGG GCAGTGGCGA GCTGTGGTGG CAGGCGGAGA GGGCTTCCTC         851
CTCCAAGTCT TGGATCACCT TTGACCTGAA GAACAAGGAA GTGTCTGTAA         901
AACGGGTTAC CCAGGACCCT AAGCTCCAGA TGGGCAAGAA GCTCCCGCTC         951
CACCTCACCC TGCCCCAGGC CTTGCCTCAG TATGCTGGCT CTGGAAACCT        1001
CACCCTGGCC CTTGAAGCGA AAACAGGAAA GTTGCATCAG GAAGTGAACC        1051
TGGTGGTGAT GAGAGCCACT CAGCTCCAGA AAAATTTGAC CTGTGAGGTG        1101
TGGGGACCCA CCTCCCCTAA GCTGATGCTG AGCTTGAAAC TGGAGAACAA        1151
GGAGGCAAAG GTCTCGAAGC GGGAGAAGCC GGTGTGGGTG CTGAACCCTG        1201
AGGCGGGGAT GTGGCAGTGT CTGCTGAGTG ACTCGGGACA GGTCCTGCTG        1251
GAATCCAACA TCAAGGTTCT GCCCACATGG TCCACCCCGG TGCACGCGGA        1301
TCCC  (SEQ ID NO: 28)
```

Amino Acid Sequence

```
MNRGVPFRHL LLVLQLALLP AATQGNKVVL GKKGDTVELT CTASQKKSIQ          51
FHWKNSNQIK ILGNQGSFLT KGPSKLNDRA DSRRSLWDQG NFPLIIKNLK         101
IEDSDTYICE VEDQKEEVQL LVFGLTANSD THLLQGQSLT LTLESPPGSS         151
PSVQCRSPRG KNIQGGKTLS VSQLELQDSG TWTCTVLQNQ KKVEFKIDIV         201
VLAFQKASSI VYKKEGEQVE FSFPLAFTVE KLTGSGELWW QAERASSSKS         251
WITFDLKNKE VSVKRVTQDP KLQMGKKLPL HLTLPQALPQ YAGSGNLTLA         301
LEAKTGKLHQ EVNLVVMRAT QLQKNLTCEV WGPTSPKLML SLKLENKEAK         351
VSKREKPVWV LNPEAGMWQC LLSDSGQVLL ESNIKVLPTW STPVHADP
(SEQ ID NO: 29)
```

FIG. 23

D1-D2 of CD4

Nucleic Acid Sequence

```
GCCTGTTTGA GAAGCAGCGG GCAAGAAAGA CGCAAGCCCA GAGGCCCTGC          51
CATTTCTGTG GGCTCAGGTC CCTACTGGCT CAGGCCCCTG CCTCCCTCGG         101
CAAGGCCACA ATGAACCGGG GAGTCCCTTT TAGGCACTTG CTTCTGGTGC         151
TGCAACTGGC GCTCCTCCCA GCAGCCACTC AGGGAAACAA AGTGGTGCTG         201
GGCAAAAAAG GGGATACAGT GGAACTGACC TGTACAGCTT CCCAGAAGAA         251
GAGCATACAA TTCCACTGGA AAAACTCCAA CCAGATAAAG ATTCTGGGAA         301
ATCAGGGCTC CTTCTTAACT AAAGGTCCAT CCAAGCTGAA TGATCGCGCT         351
GACTCAAGAA GAAGCCTTTG GGACCAAGGA AACTTCCCCC TGATCATCAA         401
GAATCTTAAG ATAGAAGACT CAGATACTTA CATCTGTGAA GTGGAGGACC         451
AGAAGGAGGA GGTGCAATTG CTAGTGTTCG GATTGACTGC CAACTCTGAC         501
ACCCACCTGC TTCAGGGGCA GAGCCTGACC CTGACCTTGG AGAGCCCCCC         551
TGGTAGTAGC CCCTCAGTGC AATGTAGGAG TCCAAGGGGT AAAAACATAC         601
AGGGGGGGAA GACCCTCTCC GTGTCTCAGC TGGAGCTCCA GGATAGTGGC         651
ACCTGGACAT GCACTGTCTT GCAGAACCAG AAGAAGGTGG AGTTCAAAAT         701
AGACATCGTG GTGCTAGCT  (SEQ ID NO: 30)
```

Amino Acid Sequence

```
MNRGVPFRHL LLVLQLALLP AATQGNKVVL GKKGDTVELT CTASQKKSIQ          51
FHWKNSNQIK ILGNQGSFLT KGPSKLNDRA DSRRSLWDQG NFPLIIKNLK         101
IEDSDTYICE VEDQKEEVQL LVFGLTANSD THLLQGQSLT LTLESPPGSS         151
PSVQCRSPRG KNIQGGKTLS VSQLELQDSG TWTCTVLQNQ KKVEFKIDIV         201
VLA (SEQ ID NO: 31)
```

FIG. 24

Hinge, CH_2, and CH_3 Domains of Human IgG1

Nucleic Acid Sequence

```
GCTAGCAGAG CCCAAATCTT GTGACAAAAC TCACACATGC CCACCGTGCC          51
CAGCACCTGA ACTCCTGGGG GGACCGTCAG TCTTCCTCTT CCCCCCAAAA         101
CCCAAGGACA CCCTCATGAT CTCCCGGACC CCTGAGGTCA CATGCGTGGT         151
GGTGGACGTG AGCCACGAAG ACCCTGAGGT CAAGTTCAAC TGGTACGTGG         201
ACGGCGTGGA GGTGCATAAT GCCAAGACAA AGCCGCGGGA GGAGCAGTAC         251
AACAGCACGT ACCGGGTGGT CAGCGTCCTC ACCGTCCTGC ACCAGGACTG         301
GCTGAATGGC AAGGAGTACA AGTGCAAGGT CTCCAACAAA GCCCTCCCAG         351
CCCCCATCGA GAAAACCATC TCCAAAGCCA AAGGGCAGCC CCGAGAACCA         401
CAGGTGTACA CCCTGCCCCC ATCCCGGGAT GAGCTGACCA AGAACCAGGT         451
CAGCCTGACC TGCCTGGTCA AAGGCTTCTA TCCCAGCGAC ATCGCCGTGG         501
AGTGGGAGAG CAATGGGCAG CCGGAGAACA ACTACAAGAC CACGCCTCCC         551
GTGCTGGACT CCGACGGCTC CTTCTTCCTC TACAGCAAGC TCACCGTGGA         601
CAAGAGCAGG TGGCAGCAGG GGAACGTCTT CTCATGCTCC GTGATGCATG         651
AGGCTCTGCA CAACCACTAC ACGCAGAAGA GCCTCTCCCT GTCTCCGGGG         701
CTGCAACTGG ACGAGACCTG TGCTGAGGCC CAGGACGGGG AGCTGGACGG         751
GCTCTGGACG ACGGATCC    (SEQ ID NO: 32)
```

Amino Acid Sequence

```
EPKSCDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD          51
VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN         101
GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR DELTKNQVSL         151
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS         201
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GLQLDETCAE AQDGELDGLW         251
TTDP  (SEQ ID NO: 33)
```

FIG. 25

CD7 Transmembrane Domain

Nucleic Acid Sequence

```
CCAAGGGCCT CTGCCCTCCC TGCCCCACCG ACAGGCTCCG CCCTCCCTGA      51
CCCGCAGACA GCCTCTGCCC TCCCTGACCC GCCAGCAGCC TCTGCCCTCC     101
CTGCGGCCCT GGCGGTGATC TCCTTCCTCC TCGGGCTGGG CCTGGGGGTG     151
GCGTGTGTGC TGGCGAGGAC GCGT  (SEQ ID NO: 34)
```

Amino Acid Sequence

```
PRASALPAPP TGSALPDPQT ASALPDPPAA SALPAALAVI SFLLGLGLGV      51
ACVLARTR  (SEQ ID NO: 35)
```

FIG. 26

Zeta Intracellular Domain

Nucleic Acid Sequence

```
ACGCGTTTCA GCAGGAGCGC AGAGCCCCCC GCGTACCAGC AGGGCCAGAA      51
CCAGCTCTAT AACGAGCTCA ATCTAGGACG AAGAGAGGAG TACGATGTTT     101
TGGACAAGAG ACGTGGCCGG GACCCTGAGA TGGGGGGAAA GCCGAGAAGG     151
AAGAACCCTC AGGAAGGCCT GTACAATGAA CTGCAGAAAG ATAAGATGGC     201
GGAGGCCTAC AGTGAGATTG GGATGAAAGG CGAGCGCCGG AGGGGCAAGG     251
GGCACGATGG CCTTTACCAG GGTCTCAGTA CAGCCACCAA GGACACCTAC     301
GACGCCCTTC ACATGCAGGC CCTGCCCCCT CGCTAAAGCG GCCGC
(SEQ ID NO: 36)
```

Amino Acid Sequence

```
TRFSRSAEPP AYQQGQNQLY NELNLGRREE YDVLDKRRGR DPEMGGKPRR      51
KNPQEGLYNE LQKDKMAEAY SEIGMKGERR RGKGHDGLYQ GLSTATKDTY     101
DALHMQALPP R  (SEQ ID NO: 37)
```

FIG. 27